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DATE: Friday, December 19, 2003

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	<i>DB=PGPB,USPT; PLUR=YES; OP=ADJ</i>		
<input type="checkbox"/>	L9	L8 and l5	3
<input type="checkbox"/>	L8	L7 and (dna or cdna or nucleotide or polynucleotide or nucleic acid)	4
<input type="checkbox"/>	L7	L6 and (prunus serotina)	7
<input type="checkbox"/>	L6	Hydroxynitrile lyase or Acetone cyanohydrin lyase or Hydroxymandelonitrile lyase or S Hydroxynitrilase or S Hydroxynitrile lyase or S Oxynitrilase or Mandelonitrile lyase or R Oxynitrilase	80
<input type="checkbox"/>	L5	L4 or l3 or l2 or l1	25233
<input type="checkbox"/>	L4	(536/23.2)! .ccls.	9972
<input type="checkbox"/>	L3	(435/320.1)! .ccls.	21758
<input type="checkbox"/>	L2	(435/232)! .ccls.	427
<input type="checkbox"/>	L1	(435/183)! .ccls.	4282

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Search Results - Record(s) 1 through 7 of 7 returned.

☐ 1. Document ID: US 20030148440 A1

L7: Entry 1 of 7

File: PGPB

Aug 7, 2003

PGPUB-DOCUMENT-NUMBER: 20030148440

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030148440 A1

TITLE: Process for producing hydroxynitrile lyases

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KMC	Draw Desc	Image
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☐ 2. Document ID: US 20030129714 A1

L7: Entry 2 of 7

File: PGPB

Jul 10, 2003

PGPUB-DOCUMENT-NUMBER: 20030129714

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030129714 A1

TITLE: Process for preparing protected, enantiomer-enriched cyanohydrins by in-situ derivatization

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KMC	Draw Desc	Image
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☐ 3. Document ID: US 20030129713 A1

L7: Entry 3 of 7

File: PGPB

Jul 10, 2003

PGPUB-DOCUMENT-NUMBER: 20030129713

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030129713 A1

TITLE: Process for preparing enantiomer-enriched cyanohydrins using acetals or ketals as substrates

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KMC	Draw Desc	Image
------	-------	----------	-------	--------	----------------	------	-----------	-----------	-------------	--------	-----	-----------	-------

☐ 4. Document ID: US 20030129712 A1

L7: Entry 4 of 7

File: PGPB

Jul 10, 2003

PGPUB-DOCUMENT-NUMBER: 20030129712

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030129712 A1

TITLE: Process for preparing heterocyclic (R)- and (S)-cyanohydrins

☐ 5. Document ID: US 20030119099 A1

L7: Entry 5 of 7

File: PGPB

Jun 26, 2003

PGPUB-DOCUMENT-NUMBER: 20030119099

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030119099 A1

TITLE: Genes containing a DNA sequence coding for hydroxynitrile lyase, recombinant proteins derived therefrom and having hydroxynitrile lyase activity, and use thereof

☐ 6. Document ID: US 20010051335 A1

L7: Entry 6 of 7

File: PGPB

Dec 13, 2001

PGPUB-DOCUMENT-NUMBER: 20010051335

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20010051335 A1

TITLE: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL

☐ 7. Document ID: US 6096545 A

L7: Entry 7 of 7

File: USPT

Aug 1, 2000

US-PAT-NO: 6096545

DOCUMENT-IDENTIFIER: US 6096545 A

**** See image for Certificate of Correction ****

TITLE: Phosphate starvation-inducible proteins

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L6 and (prunus serotina)

7

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=> s hydroxynitrile lyase/cn
L1 3 HYDROXYNITRILE LYASE/CN

=> d 1-3

L1 ANSWER 1 OF 3 REGISTRY COPYRIGHT 2003 ACS on STN
RN 112567-89-2 REGISTRY
CN Lyase, acetone-cyanohydrin (9CI) (CA INDEX NAME)
OTHER NAMES:
CN (S)-Hydroxynitrile lyase
CN .alpha.-Hydroxynitrile lyase
CN Acetone-cyanohydrin lyase
CN E.C. 4.1.2.37
CN E.C. 4.1.2.39
CN **Hydroxynitrile lyase**
MF Unspecified
CI MAN
SR CA
LC STN Files: AGRICOLA, BIOBUSINESS, BIOSIS, CA, CAPLUS, CASREACT, CIN,
TOXCENTER, USPATFULL

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
67 REFERENCES IN FILE CA (1907 TO DATE)
7 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
67 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L1 ANSWER 2 OF 3 REGISTRY COPYRIGHT 2003 ACS on STN
RN 9075-38-1 REGISTRY
CN Lyase, hydroxymandelonitrile (9CI) (CA INDEX NAME)
OTHER NAMES:
CN (S)-p-Hydroxymandelonitrile lyase
CN E.C. 4.1.2.11
CN **Hydroxynitrile lyase**
CN S-Hydroxynitrilase
CN S-Hydroxynitrile lyase
CN S-Oxynitrilase
MF Unspecified
CI MAN
LC STN Files: AGRICOLA, BIOBUSINESS, BIOSIS, CA, CAPLUS, CASREACT, CEN,
CHEMINFORMRX, CIN, PROMT, TOXCENTER, USPATFULL

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
73 REFERENCES IN FILE CA (1907 TO DATE)
2 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
74 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L1 ANSWER 3 OF 3 REGISTRY COPYRIGHT 2003 ACS on STN
RN 9024-43-5 REGISTRY
CN Lyase, mandelonitrile (9CI) (CA INDEX NAME)
OTHER NAMES:
CN E.C. 4.1.2.10
CN **Hydroxynitrile lyase**
CN Mandelonitrile lyase
CN R-Hydroxynitrile lyase
CN R-Oxynitrilase
CN R-Oxynitrilase
MF Unspecified
CI MAN
LC STN Files: AGRICOLA, BIOBUSINESS, BIOSIS, CA, CAPLUS, CASREACT,
CHEMCATS, CHEMINFORMRX, CHEMLIST, CSCHEM, IFICDB, IFIPAT, IFIUDB,
TOXCENTER, USPAT2, USPATFULL
Other Sources: EINECS**
(*Enter CHEMLIST File for up-to-date regulatory information)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
210 REFERENCES IN FILE CA (1907 TO DATE)
4 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
212 REFERENCES IN FILE CAPLUS (1907 TO DATE)

=> d full his

(FILE 'HOME' ENTERED AT 13:24:28 ON 18 DEC 2003)

FILE 'REGISTRY' ENTERED AT 13:24:33 ON 18 DEC 2003

L1 3 SEA ABB=ON PLU=ON HYDROXYNITRILE LYASE/CN
D 1-3

FILE 'HCAPLUS' ENTERED AT 13:25:00 ON 18 DEC 2003

E PRUNUS SEROTINA/CT
E E3+ALL

FILE 'REGISTRY' ENTERED AT 13:25:42 ON 18 DEC 2003

L2 SET SMARTSELECT ON
SEL PLU=ON L1 1- CHEM : 18 TERMS
SET SMARTSELECT OFF

FILE 'HCAPLUS' ENTERED AT 13:25:42 ON 18 DEC 2003

L3 378 SEA ABB=ON PLU=ON L2
L4 17 SEA ABB=ON PLU=ON L3 (L) (PRUNUS SEROTINA)
L5 16 SEA ABB=ON PLU=ON L4 AND PD<20010116
L6 6 SEA ABB=ON PLU=ON L5 AND (DNA OR CDNA OR NUCLEOTIDE OR
POLYNUCLEOTIDE OR NUCLEIC ACID)

=> d ibib ab 1-6

L6 ANSWER 1 OF 6 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1999:258627 HCAPLUS
DOCUMENT NUMBER: 131:98302
TITLE: Molecular analysis of (R)-(+)-mandelonitrile lyase
microheterogeneity in black cherry
AUTHOR(S): Hu, Zihua; Poulton, Jonathan E.
CORPORATE SOURCE: Department of Biological Sciences, The University of
Iowa, Iowa City, IA, 52242, USA
SOURCE: Plant Physiology (1999), 119(4), 1535-1546
CODEN: PLPHAY; ISSN: 0032-0889
PUBLISHER: American Society of Plant Physiologists
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The flavoprotein (R)-(+)-mandelonitrile lyase (MDL; EC 4.1.2.10), which plays a key role in cyanogenesis in rosaceous stone fruits, occurs in black cherry (*Prunus serotina* Ehrh.) homogenates as several closely related isoforms. Biochem. and mol. biol. methods were used to investigate MDL microheterogeneity and function in this species. Three novel MDL cDNAs of high sequence identity (designated MDL2, MDL4, and MDL5) were isolated. Like MDL1 and MDL3 cDNAs (Z. Hu, J.E. Poulton [1997] Plant Physiol 115: 1359-1369), they had open reading frames that predicted a FAD-binding site, multiple N-glycosylation sites, and an N-terminal signal sequence. The N terminus of an MDL isoform purified from seedlings matched the derived amino acid sequence of the MDL4 cDNA. Genomic sequences corresponding to the MDL1, MDL2, and MDL4 cDNAs were obtained by polymerase chain reaction amplification of genomic DNA. Like the previously reported mdl3 gene, these genes are interrupted at identical positions by three short, conserved introns. Given their overall similarity, we conclude that the genes mdl1, mdl2, mdl3, mdl4, and mdl5 are derived from a common ancestral gene and constitute members of a gene family. Genomic Southern-blot anal. showed that this family has approx. eight members. Northern-blot anal. using gene-specific probes revealed differential expression of the genes mdl1, mdl2, mdl3, mdl4, and mdl5.

REFERENCE COUNT: 60 THERE ARE 60 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 2 OF 6 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1998:583095 HCAPLUS
DOCUMENT NUMBER: 129:299647
TITLE: Molecular cloning of the cDNA coding for the
(R)-(+)-mandelonitrile lyase of *Prunus amygdalus*.
Temporal and spatial expression patterns in flowers
and mature seeds
AUTHOR(S): Suelves, Monica; Puigdomenech, Pere
CORPORATE SOURCE: Dep. Genetica Molecular, CID-CSIC, Barcelona, E-08034,
Spain
SOURCE: Planta (1998), 206(3), 388-393
CODEN: PLANAB; ISSN: 0032-0935
PUBLISHER: Springer-Verlag
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A gene highly expressed in the floral organs of almond (*Prunus amygdalus*) and coding for the cyanogenic enzyme (R)-(+)-mandelonitrile lyase (EC 4.1.2.10), has been identified and the full-length cDNA sequenced. The temporal expression pattern in maturing seeds and during floral development was analyzed by RNA blot, and the highest mRNA levels were detected in floral tissues. The spatial mRNA accumulation pattern in almond flower buds was also analyzed by in-situ hybridization. The mRNA levels were compared during seed maturation and floral development in fruit and floral samples from cultivars classified as homozygous or heterozygous for the sweet-almond trait or homozygous for the bitter trait. No correlation was found between these characteristics and levels of mandelonitrile lyase mRNA, suggesting that the presence of this protein is not the limiting factor in the prodn. of hydrogen cyanide.

L6 ANSWER 3 OF 6 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1997:804853 HCAPLUS
DOCUMENT NUMBER: 128:137053
TITLE: Sequencing, genomic organization, and preliminary promoter analysis of a black cherry (R)-(+)-mandelonitrile lyase gene
AUTHOR(S): Hu, Zihua; Poulton, Jonathan E.
CORPORATE SOURCE: Department of Biological Sciences, The University of Iowa, Iowa City, IA, 52242, USA
SOURCE: Plant Physiology (1997), 115(4), 1359-1369
CODEN: PLPHAY; ISSN: 0032-0889
PUBLISHER: American Society of Plant Physiologists
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The flavoprotein (R)-(+)-mandelonitrile lyase (MDL; EC 4.1.2.10) plays a key role in cyanogenesis in rosaceous stone fruits. An MDL gene (mdl3) and its corresponding cDNA (MDL3) were isolated from black cherry (*Prunus serotina*) and characterized. The mdl3 gene contains 2292 bp of the 5' flanking region, the entire coding region, and 300 bp of the 3' flanking region. The coding region is interrupted by three short introns, of which one possesses the unusual GC-AG splice junction dinucleotides. This gene encodes a polypeptide of 573 amino acids that includes a putative signal sequence, 13 potential N-glycosylation sites, and a presumptive FAD-binding site. To det. whether the 5' flanking region of the mdl3 gene is capable of driving MDL expression, it was fused to the .beta.-glucuronidase reporter gene for Agrobacterium-mediated transformation into tobacco. Matching endogenous MDL expression patterns, .beta.-glucuronidase staining was obsd. in maturing embryos and seeds; it also occurred in postembryonic tissues, esp. in assocn. with vascular tissues. After developing a homologous transient transformation system to facilitate identification of putative regulatory sequences, we demonstrated that 125 bp (-107 to +18) of the 5' flanking sequence of the mdl3 gene is sufficient for MDL expression in protoplasts derived from immature black cherry embryos.
REFERENCE COUNT: 47 THERE ARE 47 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 4 OF 6 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1997:142643 HCAPLUS
DOCUMENT NUMBER: 126:235180
TITLE: Molecular cloning of acetone cyanohydrin lyase from flax (*Linum usitatissimum*). Definition of a novel class of hydroxynitrile lyases
AUTHOR(S): Trummier, Klaus; Wajant, Harald
CORPORATE SOURCE: Institute of Cell Biology and Immunology, University of Stuttgart, Stuttgart, 70569, Germany
SOURCE: Journal of Biological Chemistry (1997), 272(8), 4770-4774
CODEN: JBCHA3; ISSN: 0021-9258
PUBLISHER: American Society for Biochemistry and Molecular Biology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Acetone cyanohydrin lyase from *Linum usitatissimum* is a hydroxynitrile lyase (HNL) which is involved in the catabolism of cyanogenic glycosides in young seedlings of flax. The authors have isolated a full-length cDNA clone encoding L. usitatissimum HNL (LuHNL) from a cDNA expression library by immunoscreening. LuHNL cDNA was expressed in *Escherichia coli* and isolated from the resp. sol. fraction in an active form which was biochem. indistinguishable from the natural enzyme. An open reading frame of 1266 base pairs encodes for a protein of 45,780 kDa. The derived amino acid sequence shows no overall homologies to the to date cloned HNLs, but has significant similarities to members of the alc. dehydrogenase (ADH) family of enzymes. In particular, the cysteine and histidine residues responsible for coordination of an active site Zn2+ and a second structurally important Zn2+ in alc. dehydrogenases are conserved. Nevertheless, the authors found neither alc. dehydrogenase activity in LuHNL nor HNL activity in ADH. Moreover, well known inhibitors of ADHs, which interfere with the coordination of the active site Zn2+, fail to

affect HNL activity of LuHNL, suggesting principally different mechanisms of cyanohydrin cleavage and alc. oxidn. Interestingly, LuHNL like ADH and *Prunus serotina* (PshNL) possesses an ADP-binding .beta..alpha..beta. unit motif, pointing to the possibility that the non-flavoprotein PshNL and the flavoprotein LuHNL have developed from two independent lines of evolution of a common ancestor with an ADP-binding .beta..alpha..beta. unit.

REFERENCE COUNT: 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 5 OF 6 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1995:811505 HCAPLUS

DOCUMENT NUMBER: 123:334898

TITLE: Temporal and spatial expression of amygdalin hydrolase and (R)-(+)-mandelonitrile lyase in black cherry seeds

AUTHOR(S): Zheng, Liansheng; Poulton, Jonathan E.

CORPORATE SOURCE: Dep. Biol. Sciences, Univ. Iowa, Iowa City, IA, 52242, USA

SOURCE: Plant Physiology (1995), 109(1), 31-9

CODEN: PLPHAY; ISSN: 0032-0889

PUBLISHER: Dekker

DOCUMENT TYPE: Journal

LANGUAGE: English

AB In black cherry (*Prunus serotina* Ehrh.) macerates, the cyanogenic diglucoside (R)-amygdalin undergoes stepwise degradn. to HCN catalyzed by amygdalin hydrolase (AH), prunasin hydrolase, and (R)-(+)-mandelonitrile lyase (MDL). A near full-length AH cDNA clone (pAH1), whose insert encodes the isoenzyme AH I, has been isolated and sequenced. AH I exhibits several features characteristic of .beta.-glucosidases of the BGA family, including their likely nucleophile center (isoleucine-threonine-glutamic acid-asparagine-glycine) and acid catalyst (asparagine-glutamic acid-proline/isoleucine) motifs. The temporal expression of AH and MDL in ripening fruit was analyzed by northern blotting. Neither mRNA was detectable until approx. 40 days after flowering (DAF), when embryos first became visible to the naked eye. Both mRNAs peaked at approx. 49 DAF before declining to negligible levels when the fruit matured (82 DAF). Taken together with enzyme activity data, these time courses suggest that AH and MDL expression may be under transcriptional control during fruit maturation. In situ hybridization anal. indicated that AH transcripts are restricted to the procambium, whereas MDL transcripts are localized within cotyledonary parenchyma cells. These tissue-specific distributions are consistent with the major locations of AH and MDL protein in mature seeds previously detd. by immunocytochem. (E. Swain, C.P.Li, and J.E. Poulton [1992] Plant Physiol 100:291-300).

L6 ANSWER 6 OF 6 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1994:47094 HCAPLUS

DOCUMENT NUMBER: 120:47094

TITLE: Cloning of cDNA of *Prunus serotina* (R)-(+)-mandelonitrile lyase and identification of a putative FAD-binding site

AUTHOR(S): Cheng, I Ping; Poulton, Jonathan E.

CORPORATE SOURCE: Dep. Biol. Sci., Univ. Iowa, Iowa City, IA, 52242, USA

SOURCE: Plant and Cell Physiology (1993), 34(7), 1139-43

CODEN: PCPHA5; ISSN: 0032-0781

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A full-length cDNA clone encoding the flavoprotein (R)-(+)-mandelonitrile lyase was isolated from a black cherry (*Prunus serotina*) cDNA expression library and sequenced. A putative FAD-binding site was identified near the N-terminus of this enzyme by comparing its deduced amino acid sequence with those of other FAD- and NAD-binding proteins.

=> d 15 ibib ab 1-16

L5 ANSWER 1 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1999:258627 HCAPLUS
DOCUMENT NUMBER: 131:98302
TITLE: Molecular analysis of (R)-(+)-mandelonitrile lyase
microheterogeneity in black cherry
AUTHOR(S): Hu, Zihua; Poulton, Jonathan E.
CORPORATE SOURCE: Department of Biological Sciences, The University of
Iowa, Iowa City, IA, 52242, USA
SOURCE: Plant Physiology (1999), 119(4), 1535-1546
CODEN: PLPHAY; ISSN: 0032-0889
PUBLISHER: American Society of Plant Physiologists
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The flavoprotein (R)-(+)-mandelonitrile lyase (MDL; EC 4.1.2.10), which plays a key role in cyanogenesis in rosaceous stone fruits, occurs in black cherry (*Prunus serotina* Ehrh.) homogenates as several closely related isoforms. Biochem. and mol. biol. methods were used to investigate MDL microheterogeneity and function in this species. Three novel MDL cDNAs of high sequence identity (designated MDL2, MDL4, and MDL5) were isolated. Like MDL1 and MDL3 cDNAs (Z. Hu, J.E. Poulton [1997] Plant Physiol 115: 1359-1369), they had open reading frames that predicted a FAD-binding site, multiple N-glycosylation sites, and an N-terminal signal sequence. The N terminus of an MDL isoform purified from seedlings matched the derived amino acid sequence of the MDL4 cDNA. Genomic sequences corresponding to the MDL1, MDL2, and MDL4 cDNAs were obtained by polymerase chain reaction amplification of genomic DNA. Like the previously reported md13 gene, these genes are interrupted at identical positions by three short, conserved introns. Given their overall similarity, we conclude that the genes md11, md12, md13, md14, and md15 are derived from a common ancestral gene and constitute members of a gene family. Genomic Southern-blot anal. showed that this family has approx. eight members. Northern-blot anal. using gene-specific probes revealed differential expression of the genes md11, md12, md13, md14, and md15.

REFERENCE COUNT: 60 THERE ARE 60 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 2 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1999:230470 HCAPLUS
DOCUMENT NUMBER: 131:28519
TITLE: The mandelonitrile lyase gene family in *Prunus serotina*
AUTHOR(S): Hu, Zihua
CORPORATE SOURCE: Univ. of Iowa, Iowa City, IA, USA
SOURCE: (1998) 196 pp. Avail.: UMI, Order No. DA9904300
From: Diss. Abstr. Int., B 1999, 59(9), 4632
DOCUMENT TYPE: Dissertation
LANGUAGE: English

AB Unavailable

L5 ANSWER 3 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1998:583095 HCAPLUS
DOCUMENT NUMBER: 129:299647
TITLE: Molecular cloning of the cDNA coding for the (R)-(+)-mandelonitrile lyase of *Prunus amygdalus*. Temporal and spatial expression patterns in flowers and mature seeds
AUTHOR(S): Suelves, Monica; Puigdomenech, Pere
CORPORATE SOURCE: Dep. Genetica Molecular, CID-CSIC, Barcelona, E-08034, Spain
SOURCE: Planta (1998), 206(3), 388-393
CODEN: PLANAB; ISSN: 0032-0935
PUBLISHER: Springer-Verlag
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A gene highly expressed in the floral organs of almond (*Prunus amygdalus*)

and coding for the cyanogenic enzyme (R)-(+)-mandelonitrile lyase (EC 4.1.2.10), has been identified and the full-length cDNA sequenced. The temporal expression pattern in maturing seeds and during floral development was analyzed by RNA blot, and the highest mRNA levels were detected in floral tissues. The spatial mRNA accumulation pattern in almond flower buds was also analyzed by in-situ hybridization. The mRNA levels were compared during seed maturation and floral development in fruit and floral samples from cultivars classified as homozygous or heterozygous for the sweet-almond trait or homozygous for the bitter trait. No correlation was found between these characteristics and levels of mandelonitrile lyase mRNA, suggesting that the presence of this protein is not the limiting factor in the prodn. of hydrogen cyanide.

L5 ANSWER 4 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1997:804853 HCAPLUS
DOCUMENT NUMBER: 128:137053
TITLE: Sequencing, genomic organization, and preliminary promoter analysis of a black cherry (R)-(+)-mandelonitrile lyase gene
AUTHOR(S): Hu, Zihua; Poulton, Jonathan E.
CORPORATE SOURCE: Department of Biological Sciences, The University of Iowa, Iowa City, IA, 52242, USA
SOURCE: Plant Physiology (1997), 115(4), 1359-1369
CODEN: PLPHAY; ISSN: 0032-0889
PUBLISHER: American Society of Plant Physiologists
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The flavoprotein (R)-(+)-mandelonitrile lyase (MDL; EC 4.1.2.10) plays a key role in cyanogenesis in rosaceous stone fruits. An MDL gene (mdl3) and its corresponding cDNA (MDL3) were isolated from black cherry (*Prunus serotina*) and characterized. The mdl3 gene contains 2292 bp of the 5' flanking region, the entire coding region, and 300 bp of the 3' flanking region. The coding region is interrupted by three short introns, of which one possesses the unusual GC-AG splice junction dinucleotides. This gene encodes a polypeptide of 573 amino acids that includes a putative signal sequence, 13 potential N-glycosylation sites, and a presumptive FAD-binding site. To det. whether the 5' flanking region of the mdl3 gene is capable of driving MDL expression, it was fused to the .beta.-glucuronidase reporter gene for *Agrobacterium*-mediated transformation into tobacco. Matching endogenous MDL expression patterns, .beta.-glucuronidase staining was obsd. in maturing embryos and seeds; it also occurred in postembryonic tissues, esp. in assocn. with vascular tissues. After developing a homologous transient transformation system to facilitate identification of putative regulatory sequences, we demonstrated that 125 bp (-107 to +18) of the 5' flanking sequence of the mdl3 gene is sufficient for MDL expression in protoplasts derived from immature black cherry embryos.

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L5 ANSWER 5 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1997:142643 HCAPLUS
DOCUMENT NUMBER: 126:235180
TITLE: Molecular cloning of acetone cyanohydrin lyase from flax (*Linum usitatissimum*). Definition of a novel class of hydroxynitrile lyases
AUTHOR(S): Trummer, Klaus; Wajant, Harald
CORPORATE SOURCE: Institute of Cell Biology and Immunology, University of Stuttgart, Stuttgart, 70569, Germany
SOURCE: Journal of Biological Chemistry (1997), 272(8), 4770-4774
CODEN: JBCHA3; ISSN: 0021-9258
PUBLISHER: American Society for Biochemistry and Molecular Biology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Acetone cyanohydrin lyase from *Linum usitatissimum* is a hydroxynitrile lyase (HNL) which is involved in the catabolism of cyanogenic glycosides in young seedlings of

flax. The authors have isolated a full-length cDNA clone encoding L. usitatissimum HNL (LuHNL) from a cDNA expression library by immunoscreening. LuHNL cDNA was expressed in Escherichia coli and isolated from the resp. sol. fraction in an active form which was biochem. indistinguishable from the natural enzyme. An open reading frame of 1266 base pairs encodes for a protein of 45,780 kDa. The derived amino acid sequence shows no overall homologies to the to date cloned HNLs, but has significant similarities to members of the alc. dehydrogenase (ADH) family of enzymes. In particular, the cysteine and histidine residues responsible for coordination of an active site Zn²⁺ and a second structurally important Zn²⁺ in alc. dehydrogenases are conserved. Nevertheless, the authors found neither alc. dehydrogenase activity in LuHNL nor HNL activity in ADH. Moreover, well known inhibitors of ADHs, which interfere with the coordination of the active site Zn²⁺, fail to affect HNL activity of LuHNL, suggesting principally different mechanisms of cyanohydrin cleavage and alc. oxidn. Interestingly, LuHNL like ADH and *Prunus serotina* (PshNL) possesses an ADP-binding .beta..alpha..beta. unit motif, pointing to the possibility that the non-flavoprotein PshNL and the flavoprotein LuHNL have developed from two independent lines of evolution of a common ancestor with an ADP-binding .beta..alpha..beta. unit.

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L5 ANSWER 6 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1995:811505 HCAPLUS
DOCUMENT NUMBER: 123:334898
TITLE: Temporal and spatial expression of amygdalin hydrolase and (R)-(+)-mandelonitrile lyase in black cherry seeds
AUTHOR(S): Zheng, Liansheng; Poulton, Jonathan E.
CORPORATE SOURCE: Dep. Biol. Sciences, Univ. Iowa, Iowa City, IA, 52242, USA
SOURCE: Plant Physiology (1995), 109(1), 31-9
CODEN: PLPHAY; ISSN: 0032-0889
PUBLISHER: Dekker
DOCUMENT TYPE: Journal
LANGUAGE: English

AB In black cherry (*Prunus serotina* Ehrh.) macerates, the cyanogenic diglucoside (R)-amygdalin undergoes stepwise degrdn. to HCN catalyzed by amygdalin hydrolase (AH), prunasin hydrolase, and (R)-(+)-mandelonitrile lyase (MDL). A near full-length AH cDNA clone (pAH1), whose insert encodes the isoenzyme AH I, has been isolated and sequenced. AH I exhibits several features characteristic of .beta.-glucosidases of the BGA family, including their likely nucleophile center (isoleucine-threonine-glutamic acid-asparagine-glycine) and acid catalyst (asparagine-glutamic acid-proline/isoleucine) motifs. The temporal expression of AH and MDL in ripening fruit was analyzed by northern blotting. Neither mRNA was detectable until approx. 40 days after flowing (DAF), when embryos first became visible to the naked eye. Both mRNAs peaked at approx. 49 DAF before declining to negligible levels when the fruit matured (82 DAF). Taken together with enzyme activity data, these time courses suggest that AH and MDL expression may be under transcriptional control during fruit maturation. In situ hybridization anal. indicated that AH transcripts are restricted to the procambium, whereas MDL transcripts are localized within cotyledonary parenchyma cells. These tissue-specific distributions are consistent with the major locations of AH and MDL protein in mature seeds previously detd. by immunocytochem. (E. Swain, C.P.Li, and J.E. Poulton [1992] Plant Physiol 100:291-300).

L5 ANSWER 7 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1995:273430 HCAPLUS
DOCUMENT NUMBER: 122:51429
TITLE: Immunocytochemical localization of prunasin hydrolase and mandelonitrile lyase in stems and leaves of *Prunus serotina*
AUTHOR(S): Swain, Elisabeth; Poulton, Jonathan E.
CORPORATE SOURCE: Dep. Biol. Sci., Univ. Iowa, Iowa City, IA, 52242, USA
SOURCE: Plant Physiology (1994), 106(4), 1285-91

PUBLISHER: American Society of Plant Physiologists
 DOCUMENT TYPE: Journal
 LANGUAGE: English

AB In macerates of black cherry (*P. serotina*) leaves and stems, (R)-prunasin is catabolized to HCN, benzaldehyde, and D-glucose by the sequential action of prunasin hydrolase (E.C. 3.2.1.21) and (R)-(+)-mandelonitrile lyase (E.C. 4.1.2.10). Immunocytochem. techniques have shown that within these organs prunasin hydrolase occurs within the vacuoles of phloem parenchyma cells. In arborescent leaves, mandelonitrile lyase was also located in phloem parenchyma vacuoles, but comparison of serial sections revealed that these two degradative enzymes are usually localized within different cells.

L5 ANSWER 8 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1994:676851 HCAPLUS

DOCUMENT NUMBER: 121:276851

TITLE: Utilization of amygdalin during seedling development of *Prunus serotina*

AUTHOR(S): Swain, Elisabeth; Poulton, Jonathan E.

CORPORATE SOURCE: Dep. Biol. Sciences, The Univ. of Iowa, Iowa City, IA, 52242, USA

SOURCE: Plant Physiology (1994), 106(2), 437-45
 CODEN: PLPHAY; ISSN: 0032-0889

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Cotyledons of mature black cherry (*P. serotina*) seeds contain the cyanogenic diglucoside (R)-amygdalin. The levels of amygdalin, its corresponding monoglucoside (R)-prunasin, and the enzymes that metabolize these cyanoglycosides were measured during the course of seedling development. During the first 3 wk following imbibition, cotyledonary amygdalin levels declined by >80%, but free hydrogen cyanide was not released to the atm. Concomitantly, prunasin, which was not present in mature, ungerminated seeds, accumulated in the seedling epicotyls, hypocotyls, and cotyledons to levels approaching 4 μmol per seedling. Whether this prunasin resulted from amygdalin hydrolysis remains unclear, however, because these organs also possess UDPG:mandelonitrile glucosyltransferase, which catalyzes de novo prunasin biosynthesis. The redn. in amygdalin levels was paralleled by declines in the levels of amygdalin hydrolase (AH), prunasin hydrolase (PH), mandelonitrile lyase (MDL), and β -cyanoalanine synthase. At all stages of seedling development, AH and PH were localized by immunocytochem. within the vascular tissues. In contrast, MDL occurred mostly in the cotyledonary parenchyma cells but also present in the vascular tissues. Soon after imbibition, AH, PH, and MDL were found within protein bodies but were later detected in vacuoles derived from these organelles.

L5 ANSWER 9 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1994:47094 HCAPLUS

DOCUMENT NUMBER: 120:47094

TITLE: Cloning of cDNA of *Prunus serotina* (R)-(+)-mandelonitrile lyase and identification of a putative FAD-binding site

AUTHOR(S): Cheng, I Ping; Poulton, Jonathan E.

CORPORATE SOURCE: Dep. Biol. Sci., Univ. Iowa, Iowa City, IA, 52242, USA

SOURCE: Plant and Cell Physiology (1993), 34(7), 1139-43
 CODEN: PCPHA5; ISSN: 0032-0781

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A full-length cDNA clone encoding the flavoprotein (R)-(+)-mandelonitrile lyase was isolated from a black cherry (*Prunus serotina*) cDNA expression library and sequenced. A putative FAD-binding site was identified near the N-terminus of this enzyme by comparing its deduced amino acid sequence with those of other FAD- and NAD-binding proteins.

L5 ANSWER 10 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1994:4491 HCAPLUS

DOCUMENT NUMBER: 120:4491
TITLE: Enzymology of cyanogenesis in rosaceous stone fruits
AUTHOR(S): Poulton, Jonathan E.
CORPORATE SOURCE: Dep. Biol. Sci., Univ. Iowa, Iowa City, IA, 52242, USA
SOURCE: ACS Symposium Series (1992),
533 (-Glucosidases), 170-90
CODEN: ACSMC8; ISSN: 0097-6156
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English

AB A review with 43 refs. Mature black cherry (*Prunus serotina*) seeds accumulate the cyanogenic diglycoside (R)-amygdalin (the .beta.-gentiobioside of (R)-mandelonitrile). Upon tissue disruption, amygdalin is rapidly catabolized to HCN and benzaldehyde by the enzymes amygdalin hydrolase, prunasin hydrolase and **mandelonitrile lyase**. These glycoproteins were purified to homogeneity and their major kinetic and mol. properties characterized. Aspects of the temporal and spatial regulation of cyanogenesis in maturing cherry fruits were investigated using monospecific polyclonal antisera raised against each of the deglycosylated proteins. The three catabolic enzymes, which first appeared within developing seeds about six weeks after flowering, were localized at the tissue and subcellular levels by colloidal gold immunocytochem. Amygdalin hydrolase and prunasin hydrolase were found specifically within protein bodies of the procambium, while **mandelonitrile lyase** was primarily located within protein bodies of the cotyledonary parenchyma cells and with lesser amts. within the procambium. Amygdalin localization, which would reveal how premature cyanogenesis is avoided in undamaged seeds, is under investigation.

L5 ANSWER 11 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1992:630166 HCAPLUS
DOCUMENT NUMBER: 117:230166
TITLE: Tissue and subcellular localization of enzymes
catabolizing (R)-amygdalin in mature *Prunus serotina*
seeds
AUTHOR(S): Swain, Elisabeth; Li, Chun Ping; Poulton, Jonathan E.
CORPORATE SOURCE: Dep. Biol. Sci., Univ. Iowa, Iowa City, IA, 52242, USA
SOURCE: Plant Physiology (1992), 100(1), 291-300
CODEN: PLPHAY; ISSN: 0032-0889
DOCUMENT TYPE: Journal
LANGUAGE: English

AB In black cherry (*Prunus serotina*) homogenates, (R)-amygdalin is catabolized to HCN, benzaldehyde, and D-glucose by the sequential action of amygdalin hydrolase, prunasin hydrolase, and **mandelonitrile lyase**. The tissue and subcellular localizations of these enzymes were detd. within intact black cherry seeds by direct enzyme anal., immunoblotting, and colloidal gold immunocytochem. techniques. The two .beta.-glucosidases are restricted to protein bodies of the procambium, which ramifies throughout the cotyledons. Although amygdalin hydrolase occurred within the majority of procambial cells, prunasin hydrolase was confined to the peripheral layers of this meristematic tissue. Highest levels of **mandelonitrile lyase** were obsd. in the protein bodies of the cotyledonary parenchyma cells, with lesser amts. in the procambial cell protein bodies. The residual endosperm tissue had insignificant levels of amygdalin hydrolase, prunasin hydrolase, and **mandelonitrile lyase**

L5 ANSWER 12 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1992:252226 HCAPLUS
DOCUMENT NUMBER: 116:252226
TITLE: Development of the potential for cyanogenesis in
maturing black cherry (*Prunus serotina* Ehrh.) fruits
AUTHOR(S): Swain, Elisabeth; Li, Chun Ping; Poulton, Jonathan E.
CORPORATE SOURCE: Dep. Bot., Univ. Iowa, Iowa City, IA, 52242, USA
SOURCE: Plant Physiology (1992), 98(4), 1423-8
CODEN: PLPHAY; ISSN: 0032-0889
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Biochem. changes related to cyanogenesis (HCN prodn.) were monitored during maturation of black cherry (*Prunus serotina*) fruits. At weekly intervals from flowering until maturity, fruits (or selected parts thereof) were analyzed for (a) fresh and dry wts., (b) prunasin and amygdalin levels, and (c) levels of the catabolic enzymes amygdalin hydrolase, prunasin hydrolase, and **mandelonitrile lyase**. During phase I (0-28 days after flowering [DAF]), immature fruits accumulated prunasin (mean: 3 μ mol/fruit) but were acyanogenic because they lacked the above enzymes. Concomitant with cotyledon development during mid-phase II, the seeds began accumulating both amygdalin (mean: 3 μ mol/seed) and the catabolic enzymes and were highly cyanogenic upon tissue disruption. Meanwhile, prunasin levels rapidly declined and were negligible by maturity. During phases II (29-65 DAF) and III (66-81 DAF), the pericarp also accumulated amygdalin, whereas its prunasin content declined toward maturity. Lacking the catabolic enzymes, the pericarp remained acyanogenic throughout all developmental stages.

L5 ANSWER 13 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1991:579400 HCAPLUS

DOCUMENT NUMBER: 115:179400

TITLE: Immunocytochemical localization of **mandelonitrile lyase** in mature black cherry (*Prunus serotina* Ehrh.) seeds

AUTHOR(S): Wu, Hua Cheng; Poulton, Jonathan E.

CORPORATE SOURCE: Dep. Bot., Univ. Iowa, Iowa City, IA, 52242, USA

SOURCE: Plant Physiology (1991), 96(4), 1329-37

CODEN: PLPHAY; ISSN: 0032-0889

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Mandelonitrile lyase (MDL, EC 4.1.2.10), which catalyzes the reversible disocn. of (R)-(+)-mandelonitrile to benzaldehyde and hydrogen cyanide, was purified to apparent homogeneity from mature black cherry (*P. serotina*) seeds by conventional protein purifn. techniques. This flavoprotein is monomeric with a subunit mol. mass of 57 kilodaltons. Glycoprotein character was shown by its binding to the affinity matrix Con A-Sepharose 4B with subsequent elution by α -methyl-D-glucoside. Upon chem. deglycosylation by trifluoromethanesulfonic acid, the mol. mass was reduced to 50.9 kilodaltons. Two-dimensional gel anal. of deglycosylated MDL revealed the presence of several subunit isoforms of similar mol. mass but differing slightly in isoelec. point. Polyclonal antibodies were raised in New Zealand white rabbits against deglycosylated and untreated MDL. Antibody titers were detd. by enzyme linked immunosorbent and dot immunobinding assays, while their specificities were assessed by Western immunoblot anal. Antibodies raised against untreated lyase recognized several proteins in addn. to MDL. In contrast, antisera raised against deglycosylated MDL were monospecific and were utilized for developmental and immunocytochem. localization studies. SDS-PAGE and immunoblotting anal. of seed proteins during fruit maturation showed that MDL first appeared in seeds shortly after cotyledons began development. In cotyledon cells of mature seeds, MDL was localized primarily in the cell wall with lesser amts. in the protein bodies, whereas in endosperm cells, this labeling pattern was reversed. N-terminal sequence data was gathered for future mol. approaches to the question of MDL microheterogeneity.

L5 ANSWER 14 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1991:225718 HCAPLUS

DOCUMENT NUMBER: 114:225718

TITLE: Purification, characterization, and immunocytochemical localization of **mandelonitrile lyase** from mature *Prunus serotina* seeds

AUTHOR(S): Wu, Hua Cheng

CORPORATE SOURCE: Univ. Iowa, Iowa City, IA, USA

SOURCE: (1990) 211 pp. Avail.: Univ. Microfilms

Int., Order No. DA9103280

From: Diss. Abstr. Int. B 1991, 51(9), 4153

DOCUMENT TYPE: Dissertation

LANGUAGE: English

AB Unavailable

L5 ANSWER 15 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1989:436548 HCAPLUS
DOCUMENT NUMBER: 111:36548
TITLE: Localization and catabolism of cyanogenic glycosides
AUTHOR(S): Poulton, Jonathan E.
CORPORATE SOURCE: Dep. Bot., Univ. Iowa, Iowa City, IA, 52242, USA
SOURCE: Ciba Foundation Symposium (1988),
140(Cyanide Compd. Biol.), 67-91
CODEN: CIBSB4; ISSN: 0300-5208
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English

AB A review with 18 refs. The catabolism of cyanogenic glycosides is initiated by cleavage of the carbohydrate moiety by one or more .beta.-glycosidases, which yields the corresponding .alpha.-hydroxynitrile. Investigation of highly purified .beta.-glycosidases from plants contg. cyanogenic disaccharides has now indicated that these compds. may be degraded via 2 distinct pathways, depending on the plant species. .beta.-Glycosidases from *Davallia trichomanoides* and *Vicia angustifolia* hydrolyzed (R)-vicianin and (R)-amygdalin at the aglycon-disaccharide bond producing mandelonitrile and the corresponding disaccharide. Alternatively, hydrolysis of cyanogenic disaccharides in *Prunus serotina*, almonds, and *Linum usitatissimum* involves stepwise removal of the sugar residues. The nature of these enzymes and of other .beta.-glycosidases responsible for hydrolysis of simple cyanogenic monosaccharides is discussed. Hydroxynitriles may decomp. either spontaneously or enzymically in the presence of a **hydroxynitrile lyase** (I) to produce HCN and an aldehyde or ketone. The major kinetic and mol. properties of I purified from species accumulating arom. and aliph. cyanogens are reviewed. Cyanogenesis occurs rapidly only after cyanogenic plant tissues are macerated, allowing glycosides access to their catabolic enzymes. The possible nature of the compartmentation which prevents cyanogenesis under normal conditions is discussed in relation to tissue and subcellular localizations of cyanogens and catabolic enzymes.

L5 ANSWER 16 OF 16 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1986:420837 HCAPLUS
DOCUMENT NUMBER: 105:20837
TITLE: Isolation and characterization of multiple forms of **mandelonitrile lyase** from mature black cherry (*Prunus serotina* Ehrh.) seeds
AUTHOR(S): Yemm, Robert S.; Poulton, Jonathan E.
CORPORATE SOURCE: Dep. Bot., Univ. Iowa, Iowa City, IA, 52242, USA
SOURCE: Archives of Biochemistry and Biophysics (1986), 247(2), 440-5
CODEN: ABBIA4; ISSN: 0003-9861
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Five multiple forms (forms 1-5) of mandelonitrile lyase (EC 4.1.2.10) which catalyze the decompn. of maldelonitrile to benzaldehyde and HCN were extensively purified from seeds of black cherry (*P. serotina*) by concanavalin A (Con A)-Sepharose 4B chromatog. and chromatofocusing. These forms were monomers which differed only slightly in mol. wt. (57,000-59,000) and pI (4.58-4.63), but heterogeneity in their carbohydrate side-chains was suggested by Con A-Sepharose 4B chromatog. The absorption spectra of the predominating forms 4 and 5 showed max. at 278, 380, and 460 nm, indicative of flavoprotein character. Detailed comparative kinetic studies of forms 4 and 5 revealed few significant differences in behavior. Both proteins showed pH optima between 6.0 and 7.0, had identical Km values (0.17 mM) for (R,S)-mandelonitrile, and retained similar activities upon storage at 4 and -20.degree.. Neither form exhibited a metal ion requirement, and both were affected similarly by metal salts, .beta.-mercaptoethanol, and SH-group reagents. Benzoic acid, p-hydroxybenzyl alc., and benzyl alc. inhibited both forms.

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SUMMARIES

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ALIGNMENTS

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VERSION AX474395.1 GI:22214001
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
1
REFERENCE Schwab,H., Glieder,A., Kratky,C., Dreveny,I., Poehlauser,P.,
Skranc,W., Mayrhofer,H., Wirth,I., Neuhofer,R. and Bona,R.

TITLE Genes coding for hydroxynitrile lyase, recombinant proteins with hydroxynitrile lyase activity and their use
JOURNAL Patent: EP 123220-A 19 17-JUL-2002;
DSM Fine Chemicals Austria Nfg GmbH & Co KG (AT)
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ORIGIN

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DB 1141 ATATATACGATTTCTGATGGAATCTCTCATGCGCAATTTGTACGCGGTAAACGAGAGT 1200

QY 1201 ATTGTTAGTGCAGGCAATCGGAACGCTTCAGCTTCTACTACTTGTAGTGGCTTGAACCA 1260
DB 1201 ATTGTTAGTGCAGGCAATCGGAACGCTTCAGCTTCTACTACTTGTAGTGGCTTGAACCA 1260

QY 1261 GAGTCTTACCTATCTCTCAACATCAAGTTGTTGACGCGAATCTTATGTTGGGCG 1320
DB 1261 GAGTCTTACCTATCTCTCAACATCAAGTTGTTGACGCGAATCTTATGTTGGGCG 1320

QY 1321 TTTGTTGATCACAATCTCGTAATTTCAATTAATTTTGGCCCAATCAATTTGAAGCC 1380
DB 1321 TTTGTTGATCACAATCTCGTAATTTCAATTAATTTTGGCCCAATCAATTTGAAGCC 1380

QY 1381 TCTGTTGTAATCTGTTTGGGCAATTAAGATGATTATTAATCAAGTTTCTGTCAGGCTG 1440
DB 1381 TCTGTTGTAATCTGTTTGGGCAATTAAGATGATTATTAATCAAGTTTCTGTCAGGCTG 1440

QY 1441 CCAATTTCCATCTCACCCCTTTAGTCTTTTCTTCAACATCTTACCCCTTCCCAATTCG 1500
DB 1441 CCAATTTCCATCTCACCCCTTTAGTCTTTTCTTCAACATCTTACCCCTTCCCAATTCG 1500

QY 1501 ACTTTGCTCATATGTTAGTCAAGTTCCAGGACCATTTGCTCATGTTCTGTGACGCTA 1560
DB 1501 ACTTTGCTCATATGTTAGTCAAGTTCCAGGACCATTTGCTCATGTTCTGTGACGCTA 1560

QY 1561 AATTCAATCATCTGACGTGAGAAATCGCTCCAAATTAATTAATTAATTAATTAATTAATTC 1620
DB 1561 AATTCAATCATCTGACGTGAGAAATCGCTCCAAATTAATTAATTAATTAATTAATTAATTC 1620

QY 1621 ACAGACCTTGTAAATTTGTTAGGCGCATGAAGAGCTTGGTCACTTATTAAGGACAAAG 1680
DB 1621 ACAGACCTTGTAAATTTGTTAGGCGCATGAAGAGCTTGGTCACTTATTAAGGACAAAG 1680

QY 1681 GCATTAGAACCATATAAGCTCGAGATGCTGCGGAATTCACGCTTCAATTAATTTGGGA 1740
DB 1681 GCATTAGAACCATATAAGCTCGAGATGCTGCGGAATTCACGCTTCAATTAATTTGGGA 1740

QY 1741 GTACCTTTGGCAGAGAACCAACAGATGATGATGCTTCCGAAACATTTTGTCTAGATAAT 1800
DB 1741 GTACCTTTGGCAGAGAACCAACAGATGATGATGCTTCCGAAACATTTTGTCTAGATAAT 1800

QY 1801 GTAGCTTCATCTGCGCATTAACGAGTGGAGGCTTGTGGGAAGTGTGTGATGACAGT 1860
DB 1801 GTAGCTTCATCTGCGCATTAACGAGTGGAGGCTTGTGGGAAGTGTGTGATGACAGT 1860

QY 1861 TTCCGTTGTTAGGGATCAAGGATTAACGCTTGTGATGCTTCCACTTTCCCTTACGAA 1920
DB 1861 TTCCGTTGTTAGGGATCAAGGATTAACGCTTGTGATGCTTCCACTTTCCCTTACGAA 1920

QY 1921 CCAACAGCCATCTCAGGCTTCTATCTGATGTTAGGAAGTATGATGACACATTC 1980

Db	1081	GTTTAGTTTGACAAATAATTAAAGCTATTCTCTAATGCAGATTGTGACGCTATTGGAGTC	1141
Qy	1141	ATATATACGAGTTCGTAGTGAAGACTCTCATCAGGCATTTCTACGGGTACGAGAGTT	1200
Db	1141	ATATATACGAGTTCGTAGTGAAGACTCTCATCAGGCATTTCTACGGGTACGAGAGTT	1200
Qy	1201	ATTGTTAGTGCAGGACAANTCGGAACGCTCAGCTTCTACTTACTTGTGCGTGTGAACCA	1260
Db	1201	ATTGTTAGTGCAGGACAANTCGGAACGCTCAGCTTCTACTTACTTGTGCGTGTGAACCA	1260
Qy	1261	GAGCTTTACCTATCTCTCTCAACATCAGAGTGTGTCAGCGAATCTTATGTTGGCAG	1320
Db	1261	GAGCTTTACCTATCTCTCTCAACATCAGAGTGTGTCAGCGAATCTTATGTTGGCAG	1320
Qy	1321	TTTGTGTATGACAAATCCTCGTAAATTTTCATTAATATTTTGGCCCCCAATCCAAATGAGCC	1380
Db	1321	TTTGTGTATGACAAATCCTCGTAAATTTTCATTAATATTTTGGCCCCCAATCCAAATGAGCC	1380
Qy	1381	TCGTGTGAATCTGTTTTAGGCATTAGAAGTGAATTAATATCAAGTTTCTCTGTCAAGCTTG	1440
Db	1381	TCGTGTGAATCTGTTTTAGGCATTAGAAGTGAATTAATATCAAGTTTCTCTGTCAAGCTTG	1440
Qy	1441	CCATTTTCCACTCCACCCCTTTAGTCTTTTCTTCTACAACTCTTACCCCTCCCAAAATTCG	1500
Db	1441	CCATTTTCCACTCCACCCCTTTAGTCTTTTCTTCTACAACTCTTACCCCTCCCAAAATTCG	1500
Qy	1501	ACTTTTCTCATATGTTAGCCAGTTCGAGGACCATGTCATGTTCTGTGCACGCTA	1560
Db	1501	ACTTTTCTCATATGTTAGCCAGTTCGAGGACCATGTCATGTTCTGTGCACGCTA	1560
Qy	1561	AATTCATCATCTGACGTGAGAAATCGCTCCAAAATTAATAATCAATTAATCAATTAATTC	1620
Db	1561	AATTCATCATCTGACGTGAGAAATCGCTCCAAAATTAATAATCAATTAATCAATTAATTC	1620
Qy	1621	ACGAGCTTCTGCTAATTTGTGTAGCGGCATGAAGAAGCTTGGTGACTTATTAAGACAAAG	1680
Db	1621	ACGAGCTTCTGCTAATTTGTGTAGCGGCATGAAGAAGCTTGGTGACTTATTAAGACAAAG	1680
Qy	1681	GCATTAGAACCATATAAAGCTCGAGATGTCTCGGAAATTCACGGTTCATTAATTGGGA	1740
Db	1681	GCATTAGAACCATATAAAGCTCGAGATGTCTCGGAAATTCACGGTTCATTAATTGGGA	1740
Qy	1741	GTACCTTTGCCAGAACCAACAGATGATGCATCCTTCGAAACATTTTCTCTAGATAAT	1800
Db	1741	GTACCTTTGCCAGAACCAACAGATGATGCATCCTTCGAAACATTTTCTCTAGATAAT	1800
Qy	1801	GTAGCTTCATATCGGCATTACACGGGTGGAAGCCCTGTTGGGAAAGTCTTGTATGACAGT	1860
Db	1801	GTAGCTTCATATCGGCATTACACGGGTGGAAGCCCTGTTGGGAAAGTCTTGTATGACAGT	1860
Qy	1861	TTCCGTGTTATGGGGATCAAGCANTTACGGTGTGTCATGCTCCACTTCCCTTACGAA	1920
Db	1861	TTCCGTGTTATGGGGATCAAGCANTTACGGTGTGTCATGCTCCACTTCCCTTACGAA	1920
Qy	1921	CCAAACAGCCATCTCAGGCTTCTATCTGATGTTAGGAAAGTATGTGATGACACCTTC	1980
Db	1921	CCAAACAGCCATCTCAGGCTTCTATCTGATGTTAGGAAAGTATGTGATGACACCTTC	1980
Qy	1981	AACCACTAGAGATTTCTCAATTTTGTGTTGTTGTAATGAATCTCTCTCGCGCATTTGCTC	2040
Db	1981	AACCACTAGAGATTTCTCAATTTTGTGTTGTTGTAATGAATCTCTCTCGCGCATTTGCTC	2040
Qy	2041	TTTTTTTAAATCTTAAATTTTGTGTTTGGCAGGTATGTGGGCTTCAAAATCTCTC	2100
Db	2041	TTTTTTTAAATCTTAAATTTTGTGTTTGGCAGGTATGTGGGCTTCAAAATCTCTC	2100
Qy	2101	AAGAAAGGTCAATCCGGTGTGAGGCTATTTCATATAATTTCAAGAGTCCATGTGAAGATTC	2160
Db	2101	AAGAAAGGTCAATCCGGTGTGAGGCTATTTCATATAATTTCAAGAGTCCATGTGAAGATTC	2160
Qy	2161	CG 2162	
Db	2161	CG 2162	

RESULT 3	PLN 07-OCT-1996
PAMDL1	linear
LOCUS	1965 bp mRNA
DEFINITION	P.amygdalus mRNA for mandelonitrile lyase.
ACCESSION	Y08211
VERSION	Y08211.1 GI:1561640
KEYWORDS	mandelonitrile lyase; MDL1 gene.
SOURCE	Prunus dulcis (almond)
ORGANISM	Prunus dulcis
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosid I; Rosales; Rosaceae; Amygdaloideae; Prunus.
AUTHORS	1 Suelves,M.
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1965)
AUTHORS	Suelves,M.
TITLE	Direct Submission
JOURNAL	Submitted (18-SEP-1996) M. Suelves, C.I.D-C.S.I.C, Genetica Molecular, Jordi Girona 18-26, 08034 Barcelona, SPAIN
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polyA_signal	1883..1888
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	/evidence=not_experimental
BASE COUNT	558 a 400 c 400 g 607 t
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Query Match	59.4%; Score 1285.2; DB 8; Length 1965;
Best Local Similarity	86.3%; Pred. No. 8e-283;
Matches 1521; Conservative	0; Mismatches 38; Indels 203; Gaps 1;
Qy	207 TTTAGATGATGTTTGAAAAAATCTTTTCATCTTCCACATATATTTTCAGATTTTAGCT 266
Dd	63 TTCTCTTCAATTCAGAGTTTCACTCGTTCCTCAATCTTCTGCTCATGATTTTAGCT 122
Qy	267 ACTTGAAGTTTGTTGTAACGCCCACTGATACAGCTCGGAAGGATCATATGACTCATTTG 326

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Db 123 ACTTGAAGTTGTGTACAAGCCCACTGATACAAAGCTTGGAGGATCATATGACTACATTG 182
QY 327 TAATCGGTGAGGAACATCAGGCTGTCATTTGCGAGCAACTTTATCAGAAAATACAGG 386
Db 183 TAATCGGTGAGGAACATCAGGCTGTCATTTGCGAGCAACTTTATCAGAAAATACAGG 242
QY 387 TGCTTCTTCTAGAAAGGCACTATTGCTACAGAAATACCGGAACAGCTTGACTGCGAGATG 446
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QY 447 GGTITGCAATATCTGCGAGCAACAGATGATGAAAGAGCCAGCTTGAAGGTTCTGTGT 506
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QY 507 CCGAAGATGCAATGATAATGTGGAGCGAGGATCTCGGTGCGAGCCAGCATATCAATG 566
Db 363 CCGAAGATGCAATGATAATGTGGAGCGAGGATCTCGGTGCGAGCCAGCATATCAATG 422
QY 567 CAGCGCTACGCGAGAGCTAAACATTTCAATCTATAGTCAAAAGAGGATTTGAATGGGACC 626
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Db 483 TGGATTTGTCATTAAGACATATGAGTGGGTGAGAGCGCATTTGGTCAAGCCAAATA 542
QY 687 ATCAATCTTGGCAATCTGTTATAGGAGGAGGATTTCTTGGAGGCGGTATTTCTTCCAGACA 746
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Db 774 ----- 773
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QY 1227 GCCTCAGCTTCTACTTACTTGTAGTGGCTTGGACAGAGTCTTACTTCTTCTCTCAACAT 1286
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QY 1287 CACAGTTGTTTTCAGCCGAATCTTATGTTGGCGAGTTTGTGTAGCAATCTCTGTAATTT 1346
Db 940 CACAGTTGTTTTCAGCCGAATCTTATGTTGGCGAGTTTGTGTATACACACCTCTGTAATTT 999
QY 1347 CATTAATATTTTGGCCCCCAATCCAAATGGAAGCTCTGTTGTAACTGTTTGAAGCAATTAG 1406
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QY 1407 RAGTGATTAATATCAAGTTTCTCTCTCAAGCTTGCATTTTCCACTCCACCCCTTTAGTCT 1466
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QY 1467 TTTTCTCTACAAATCTTACCCCTCCCAAAATTCGACTTTTGTCTCATATTTGTTAGCCAAAT 1526
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QY 1707 TGTGCTGGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1766
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QY 1827 TGGAAAGCTTGTGGAAGAGTCTTGTGATGACAGATTTCCGTGTTATGGGATCAAAAGCAAT 1886
Db 1480 TGGAAAGCTTGTGGAAGAGTCTTGTGATGACAGATTTCCGTGTTATGGGATCAAAAGCAAT 1539
QY 1887 AGCGTGTGTTGATGCTCCACTTTCCTTCGAAACAAAGCAATCTCAGGCTTCTA 1946
Db 1540 AGCGTGTGTTGATGCTCCACTTTCCTTCGAAACAAAGCAATCTCAGGCTTCTA 1599
QY 1947 TCTGATGTTAGGAAGTATGTG 1968
Db 1600 TCTGATGTTAGGAAGTATGTG 1621
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RESULT 4

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AX474397
LOCUS AX474397 1632 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 21 from Patent EP1223220.
ACCESSION AX474397
VERSION AX474397.1 GI:22214002
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Schwab, H., Glieder, A., Kratky, C., Breveny, I., Poechlauser, P.,
Skranc, W., Mayrhofer, H., Wirth, I., Neuhofer, R. and Bona, R.
TITLE Genes coding for hydroxymethylase, recombinant proteins with
JOURNAL hydroxymethylase activity and their use
Patent: EP 1223220-A 21 17-JUL-2002;
DSM Fine Chemicals Austria Nfg GmbH & Co KG (AT)
FEATURES
Location/Qualifiers
1..1632
/organism="synthetic construct"
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/db_xref="taxon:32630"
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BASE COUNT 451 a 357 c 361 g 463 t
ORIGIN
Query Match 58.8%; Score 1272; DB 6; Length 1632;
Best Local Similarity 88.0%; Pred. No. 8.4e-280;
Matches 1485; Conservative 0; Mismatches 0; Indels 203; Gaps 1;
QY 281 TACAAGCCACTGTATACAAAGCTCGGAAGGATCATATGACTATCTATGTAATCGGTGGAGA 340
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Db      94  TACAAAGCCACTATACAAAGCTCGGAAGGATCATATGACTACATTTGTAATCGGTGGAGGA 153
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QY      401  AGAGGCATATTTGCTACAGAAATCCCGAACACCTTGACTGCGAGATGGTTTGCATATAAT 460
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QY      521  GATAAATGTGCGAGCGAGATCTCGGTGGCAGCACCATAATCAATCAGGCGCTTACGCC 580
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QY      761  GATCAGCAAGCAGGACTAGACATCACCGGCTCACTTTTGCACAAATATGAAAGCGGACAT 820
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QY      821  GCGGCTGATGAACCTGCTTAATAAGGAGACCCCTAATAACTTGTAGTTGCGAGTTCAAGCC 880
Db      634  GCGGCTGATGAACCTGCTTAATAAGGAGACCCCTAATAACTTGTAGTTGCGAGTTCAAGCC 693
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Db      694  TCAGTAGAAGATCTCTTCTCTTCCAAATACATCA----- 730
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QY      1061  AACTTCCCAATCTCTCTGTTAGTTTGAACAATAATATAAGTATTCTCTAATGCGAG 1120
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QY      1121  ATTTGTCAGCTATTGGAGTCAATATACGGTTCTGATGGAATCTCTCATCGGCAATTTG 1180
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QY      1181  TACCGGTAACGGAGAGATTATTGTTAGTGCAGGACAAATCGGAACCGCTCAGCTTCTAC 1240
Db      791  TACCGGTAACGGAGAGATTATTGTTAGTGCAGGACAAATCGGAACCGCTCAGCTTCTAC 850
QY      1241  TACTTAGTGGGTTGACCGAGTCTTACCTATCTTCTCAACATCACAGTTGTTGACG 1300
Db      851  TACTTAGTGGGTTGACCGAGTCTTACCTATCTTCTCAACATCACAGTTGTTGACG 910
QY      1301  CGAATCCTTAGTTGGGCGAGTTTGTATGACAAATCTCGTAAATTTCAATTAATTTTC 1360
Db      911  CGAATCCTTAGTTGGGCGAGTTTGTATGACAAATCTCGTAAATTTCAATTAATTTTC 970
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Db      1031  AAGTTTCTCTCAAGCTTGCATTTTCCACTCCACCTTTAGTCTTTTCTTCTACAAAT 1090
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QY      1541  CTCATGGTCTCTGCAAGCTAAATTCATCATCTGACGCTGAGAAATCGTCCAAATTTAAAT 1600
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Db      1571  GGTATGTG 1578

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RESULT 5

BD181913

LOCUS

DEFINITION

Novel gene containing DNA sequence encoding hydroxynitrile lyase,

recombinant protein originating in the gene and having

hydroxynitrile lyase activity and utilization thereof.

ACCESSION

BD181913.1

VERSION

JP 2002330791-A/20.

KEYWORDS

synthetic construct

SOURCE

artificial sequences.

ORGANISM

1 (bases 1 to 1632)

REFERENCE

Schwab,H., Greider,A., Kratky,C., Drefeny,I., Bon,R., Pehirawel,P.,

Scharnke,W., Milofar,H., Viruto,I. and Noyhoffar,R.

TITLE

Novel gene containing DNA sequence encoding hydroxynitrile lyase,

recombinant protein originating in the gene and having

hydroxynitrile lyase activity and utilization thereof

JOURNAL

Patent: JP 2002330791-A 20 19-NOV-2002;

DSM FINE CHEMICALS AUSTRIA NFG GMEH AND CO KG

COMMENT

OS Artificial Sequence

PN JP 2002330791-A/20

PF 11-JAN-2002 JP 2002005090

PR 16-JAN-2001 AT A60/2001.03-APR-2001 AT A523/2001 PI

HELMUT SCHWAB,ANTON GREIDER,CHRISTOPH KRATKY,INGREET DREFENY, PI

RUDOLPH BONA,

PI PETER PEHIRAWEL, WOLFGANG SCHARNKE, HERBERT

MILFOFAR, ILMIA VIRUTO,

PI RUDOLPH NOYHOFFAR

PC C12N15/09,C07K19/00,C12N9/04,C12N9/88,C12P13/00,C12N15/00 CC
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Location/Qualifiers
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BASE COUNT 451 a 357 c 361 g 463 t
ORIGIN
Query Match 58.8%; Score 1272; DB 6; Length 1632;
Best Local Similarity 88.0%; Pred. No. 8.4e-280;
Matches 1485; Conservative 0; Mismatches 0; Indels 203; Gaps 1;
QY 281 TACACGCCACGATACAGCTCGGAAGGATCATATGACTCATATGTAATCGGTGGAGGA 340
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DB 154 ACATCAGGGTGCCATTTGCGAGCAACTTTATCAGAAAAATACAGGTGCTTCTCTAGAA 213
QY 401 AGAGGCACTATTGCTACAGAAATACCGGAACACGTTGACTGCGAGATGGTTTGCATTAAT 460
DB 214 AGAGGCACTATTGCTACAGAAATACCGGAACACGTTGACTGCGAGATGGTTTGCATTAAT 273
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DB 274 CTGACGCAACAGATGATCGGAAGACGCGAGTTGAAAGGTTGCTGTCGGAAGATGGCAAT 333
QY 521 GATAATGTCGAGCCAGGATCTCGGTGGCAGCAACATTAATCAATGCGAGCGCTACGACC 580
DB 334 GATAATGTCGAGCCAGGATCTCGGTGGCAGCAACATTAATCAATGCGAGCGCTACGACC 393
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DB 394 AGAGCTAACATTTCTATTAGTCAACAGGAAATGGAATGGACCTGGAATTTGTCAT 453
QY 641 AAGACATATGAGTGGGTGGAAGACGCTTGTGCTCAAGCAAAATCAATCAATCTTGGCAA 700
DB 454 AAGACATATGAGTGGGTGGAAGACGCTTGTGCTCAAGCAAAATCAATCAATCTTGGCAA 513
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QY 821 CGGGCTGATGAATCTGTTAATAAGGAGACCCCTTAATACTTGTAGTTCAGTTACAGGCC 880
DB 634 CGGGCTGATGAATCTGTTAATAAGGAGACCCCTTAATACTTGTAGTTCAGTTACAGGCC 693
QY 881 TCAGTGAAGAGATCTCTTCTCTTCAATCAATCAAGTATGTTGCATCAGTGATTTTA 940
DB 694 TCAGTGAAGAGATCTCTTCTCTTCAATCAATCAAGTATGTTGCATCAGTGATTTTA 730
QY 941 ATGCTAGCTCTAGTTGTCATGCTGCATCGCAAAATTTATTTTATCATTTTAAATA 1000
DB 731 ----- 730
QY 1001 CTAACAGATAGTGTGAAGTCTCATATTTCCCTTCCATATTTCCCAAAATTTCCATAAACA 1060
DB 731 ----- 730
QY 1061 AAACCTCCCAATCTCTCTCTGTTAGTTGACAAATAATTAAGCTATTCTCTTAATGCGAG 1120
DB 731 ----- 730

QY 1121 ATTTGTGAGCTATTGGAGTCATATATACGATTTCTGATGGAAACTCTCATCAGSCATTTG 1180
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QY 1181 TACGCGGTAAACGGAAGAGTTATTGTTAGTCAGGAGCAATCGGAACGCCCTCAGCTTCTAC 1240
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DB 1031 AAGTTTCTGTCGAAGCTTGCATTTCCACTCCACCCCTTTAGTCTTTTCTTACACAT 1090
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DB 1331 ACGGTTTCAATTTATTTGGGAGTACCTTTGGCAGAGAAACCAACAGATGATGATCTTCG 1390
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DB 1511 CCTCCATTTCCCTTACGAACCAACAGCCATCTCTAGGGCTTCTATCTGATGTTAGAA 1570
QY 1961 GGTATGTG 1968
DB 1571 GGTATGTG 1578
RESULT 6
PSU78814
LOCUS
DEFINITION
Prunus serotina (R)-(+)-mandelonitrile lyase isoform MDL1 precursor
gene, complete cds.
ACCESSION
U78814
VERSION
U78814.1 GI:1730331
KEYWORDS
Prunus serotina (black cherry)
Prunus serotina
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.

1 (bases 1 to 2247)
Hu.Z. and Poulton, J.E.

Prunus serotina (R)-(+)-mandelonitrile lyase isoform MDL1 precursor
gene

Unpublished (1996)

2 (bases 1 to 2247)
Hu.Z. and Poulton, J.E.

Direct Submission

Submitted (19-NOV-1996) Biological Sciences, The University of
Iowa, Iowa City, IA 52242, USA

Location/Qualifiers

1..2247
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/mol_type="genomic DNA"
/db_xref="taxon:23207"

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GTHAADELLKNGNNLRVGVHSAVERKIIIFNAPGLTATGTVYRDSNTPHRAFVR
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BASE COUNT 633 a 472 c 463 g 679 t

ORIGIN

Query Match 56.5%; Score 1222; DB 8; Length 2247;

Best Local Similarity 76.8%; Pred. No. 2.1e-268;

Matches 1635; Conservative 0; Mismatches 405; Indels 90; Gaps 8;

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8 ATCAAAATGAGAGAAATCAACAATGTCAGTTATATCTATTGTTGTCATCTCTTGT 67

64 CTTTCATCTTCAGTATTCAGAGTTTCACTCGCTTGGCAATATCTTCGCTCATGGTAAATTT 123

68 CTCCTTCTTCAATATCTGAGGTCCACTCGCTTGGCCAGCACTTCAATCATGGTAAATCA 127

124 CCATCTTCAGTATTCATTAACAGCAAA--ATGTGTAGATTTATTAATTAAGAAACTGAC 181

128 CTTTCATCGTAAATTCAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGTGA 187

182 ACAAGTAGTGCAGAAACAGCTAAATTTAGATGATGTTTGAATAAATCTTTCA-----T 236

188 AGAAACAGCAGATATAGAGCCCTGCTAGATGATGATGATGATGATGATGATGATGAT 247

237 CTTTCACATATATTTGAGATTTAGTACTGTTGAAGTTTGTGTAACAGCCATGATA 296

248 TCGTCTCTTGGAGATTTTGCAGATTTTGTGCTACCTGAGATTTGTCATGAGCCGCTGATC 307

297 CAAGCTCGGAAGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 356

308 TAGAGTTGAGAGATCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 367

357 TGGCAGCACTTTATCAGAAATAATACAGGTGCTTCTTCTAGAAAGAGGCACTATTGCTA 416

368 TGGCAGCACTTTATCAGAAATAATACAGGTGCTTCTTCTAGAAAGAGGCACTATTGCTA 427

417 CAGAAATACCGAACAGCTTGCATGCGAGATGGGTTTGCATATATATCTGCGCAACAAGATG 476

428 CAGCATATCCCAAGCTTGCATGCGAGATGGGTTTGCATATATATCTGCGCAACAAGATG 487

477 ATGGAAGAGCCAGGTTGAAGGTTGCTGTCGCAAGATGGCATTTGATATGTCGAGGCCA 536

488 ATGGAAGAGACACCGTTCGAAGGTTTCTGTCGCAAGATGTTGTTATACGTACGCGGCA 547

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548 GGGTGTCTCGTGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 607

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1077 CTTGTTAGTTTGCACAAATATTAAGCTATTTCTTAATGACAGATTTGTGAGCTATTGG 1136

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 Db 1563 TCCGACAGATCTTCTCATTTGTTAGCGCATGAGAAAGATTTGTTGAACTCTGAGCAC 1622
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 Db 1683 GGGATCCCTTTGCCAAGGACCAACAGATGATGATGATCCTTCGAAACATTTTGCAGAG 1742
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 QY 1857 CAGTTTCCTGTTATGGGATCAAGCATTAACCGTTTGTGATGCTCCACTTTCCCTTA 1916
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 QY 1917 CGAACCAACAGCATCTCTCAGGCTTCTATCTGATGATGATGATGATGATGATGATG 1974
 Db 1863 CACACAGCGAGCACCTCAGGCTTCTATCTGATGATGATGATGATGATGATGATGATG 1922
 QY 1975 --ACTTCCACCACTAGAGATTTCTCATATTTGTTG-----TTGTTGTAATGA 2021
 Db 1923 TTAATTCGACCACTACAATTTGATTAATTAATTTGTTGTTGTTGTTGTTGTTGTTG 1982
 QY 2022 ACTCTCTGCGGCTTCTCTTTTATTAATCTTAAATTTTGTGTTTGTGTTGTTGTTGTTG 2081
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 QY 2082 GTGGGCTTCAAAATCTCGAAGAGTCA 2111
 Db 2040 GTGGGCTTAAATTTCTGCAAGAGATCA 2069

RESULT 7
 AF412329 2087 bp DNA linear PLN 08-OCT-2001
 LOCUS Prunus dulcis R-oxynitrile lyase isoenzyme 1 precursor (hnl1) gene, complete cds.
 DEFINITION
 AF412329
 AF412329.1 GI:15982975
 Prunus dulcis (almond)
 Prunus dulcis
 Prunus dulcis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
 1 (bases 1 to 2087)
 Dreveny, I., Gruber, K., Glieder, A., Thompson, A. and Kratky, C.
 The Hydroxynitrile Lyase from Almond: A Lyase that Looks Like an Oxidoreductase
 Structure Fold, Des. 9, 803-815 (2001)
 2 (bases 1 to 2087)
 Glieder, A.S., Dreveny, I., Mandl, H., Majer, S. and Schwab, H.
 Direct Submission
 Submitted (22-AUG-2001) Inst. of Biotechnology, TU-Graz,
 Petersgasse 12, Graz 8010, Austria
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 Best Local Similarity 76.3%; Pred. No. 5.2e-264;
 Matches 1605; Conservative 0; Mismatches 417; Indels 82; Gaps 7;
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 QY 133 GTATTCATTTAAGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 192
 Db 120 GTATTCATTTAAGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 179
 QY 193 AAGAAACAGCTAATTTAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 247
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 QY 248 TATTTTGAGATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 307
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 QY 368 TTATCAGAAAATACAGGCT 427
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 QY 488 CCAGTTGAAAGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 547
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 Db 540 GGCACGACATAATCAATGACAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 599
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 Db 600 TCAGAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 659
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 QY 1868 TTAGGGGATCAAGCATTAACGAGTCTTGATGACAGTTCCGCG 1927
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 QY 1928 GCCATCCTCAGGCTCTATCTGATGATGAGGAGTATGATGACAGTTCCGCG 1987
 Db 1855 GCCATCCTCAGGCTCTATCTGATGATGAGGAGTATGATGACAGTTCCGCG 1906
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 Db 1907 ATAATTATTGTTGATGCTGTTGTTGTAATGAATCTCTGCGCATGCTCTTTTAA 1966
 QY 2048 TTAATCCTTAAATTTGTTGTTGCGAGGATGATGAGGCTCTCAATCCTCGAAG 2107
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 Db 2024 ATCA 2027

RESULT 10

AF053886

LOCUS

DEFINITION Prunus serotina (R)-(+)-mandelonitrile lyase isoform MDL5 precursor (MDL5) mRNA, complete cds.

ACCESSION

AF053886

VERSION

AF053886.1

KEYWORDS

Prunus serotina (black cherry)

SOURCE

Prunus serotina

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.

REFERENCE

1 (bases 1 to 2243)

Hu, Z. and Poulton, J.E.

Direct Submission

Submitted (17-MAR-1998) Biological Sciences, The University of Iowa, Iowa City, IA 52242, USA

JOURNAL

Location/Qualifiers

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BASE COUNT 656 a 449 c 434 g 704 t

ORIGIN

Query Match 55.6%; Score 1202; DB 8; Length 2243;
 Best Local Similarity 83.4%; Pred. NO. 7.9e-264;
 Matches 1469; Conservative 0; Mismatches 90; Indels 203; Gaps 1;

QY 207 TTTAGATCGATGTTGAAAAAATCTTTCATCTCTTCACATATATTTTGCAGATTTAGCT 266
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 (MDL4) gene, complete cds.
 ACCESSION
 AF053885
 VERSION
 AF053885.1 GI:3676470
 KEYWORDS
 Prunus serotina (black cherry)
 ORGANISM
 Prunus serotina
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
 REFERENCE
 1 (bases 1 to 2380)
 Hu, Z. and Poulton, J. E.
 AUTHORS
 Direct Submission
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 Submitted (17-MAR-1998) Biological Sciences, The University of
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 Iowa, Iowa City, IA 52242, USA
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BASE COUNT 677 a 478 c 489 g 736 t
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DB	1631	TAGCGGATGAAGAAATTTGGTGTCTTCTGAGTACAGAGCAATTAAGCAATATAAGT	1690
QY	1701	TCGAGATGTCGGGAATTCAGGTTTCAATTTATTTGGGAGTACCTTTTGGCAGGAACCA	1760
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LOCUS Prunus serotina (R)-(+)-mandelonitrile lyase isoform MDL2

DEFINITION precursor, gene, complete cds.

ACCESSION AF040079

VERSION AF040079.1 GI:2773275

KEYWORDS Prunus serotina (black cherry)

SOURCE Prunus serotina

ORGANISM Prunus serotina

REFERENCE 1 (bases 1 to 2278)

AUTHORS Hu, Z. and Poulton, J.E.

TITLE Prunus serotina (R)-(+)-mandelonitrile lyase isoform MDL2 precursor gene, complete cds

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2278)

AUTHORS Hu, Z. and Poulton, J.E.

TITLE Direct Submission

JOURNAL Submitted (24-DEC-1997) Biological Sciences, The University of Iowa, Iowa City, IA 52242, USA

FEATURES

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RESULT 15
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LOCUS
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ACCESSION AF013161
VERSION AF013161.1 GI:2343180
KEYWORDS Prunus serotina (black cherry)
ORGANISM Prunus serotina
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
Hu, Z. and Poulton, J.E.
Prunus serotina (R)-(+)-mandelonitrile lyase isoform MDL3
precursor, mRNA, cds
Unpublished
2 (bases 1 to 1948)
Hu, Z. and Poulton, J.E.
Direct Submission
Submitted (09-JUL-1997) Biological Sciences Department, The
University of Iowa, Iowa City, IA 52242, USA
LOCATION/Qualifiers
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Best Local Similarity 72.88; Pred. No. 7.2e-196;
Matches 1283; Conservative 0; Mismatches 276; Indels 203; Gaps 1;

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Qy      327  TAATCGGTGGAGAAACATCAGGGTGTCCATTGGCAGCAACTTTTATCAGAAAAATACAAGG 386
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Qy      387  TCGTCTTCTTACAGAGGACCATTTGCTTACAGATACCCGACACGTTGCTGACATG 446
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Db      248  TCGTGTGTTCTAGAAAAGGGGCGCTCTTCTTACAGAAATATCCAAACCTCTTTGATATCAGATG 307
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Db      308  GGTTTGTATATATCTCCAGCAAGAGATGATGGAAGACACCAAGTCGAAGGTTTCGTTT 367
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Qy      507  CCGAAGATGGCATTTGATTAATGTGCGAGCCAGGATCCTCGGTGGCAGCACCAATTAATG 566
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Db      368  CCGAAGATGGTATTGATAACGTACGGGCGAGGGTCTTGGTGGCAACAAGCATGATCAATG 427
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Qy      567  CAGGCGTCTACCCAGAGCTAATTTCTTCTATAGTCMAACAGGATTTGATGCGGACC 626
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Db      776  -----CAGGTGTGACAGCTATAGGAGTTATATATACTGATTCGAATGGAACGAC 824
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Db      825  TCATCAGGCATTTGTACCGGTGAGGAGAAAGTTATATTGAGTCAGGCGCAATGGGTC 884
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Db	1605		

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Job time : 7878 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2003, 15:05:47 ; Search time 4526 Seconds
(without alignments)
11609.871 Million cell updates/sec

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Perfect score: 2162
Sequence: 1 ggaattcacaatggagaa.....agtcctatggaagaattccg 2162

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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29:	gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	451.8	20.9	639	13	BUS74120 PA_Ea000
3	438.6	20.3	654	13	BUS75280 PA_Ea000
4	423.6	19.6	648	13	BUS74474 PA_Ea000

5	394.6	18.3	640	13	BUS75069
6	392	18.1	658	13	BUS72973
7	383.4	17.7	598	13	BUS64516
8	375.8	17.4	656	13	BUS72692
9	358.2	16.6	634	13	BUS74792
10	317.2	14.7	626	13	BUS74699
11	314.8	14.6	505	13	BUS74357
12	242.6	11.2	621	13	BUS74592
13	242.6	11.2	622	13	BUS74379
14	185.4	8.6	543	13	BUS72781
15	143.8	6.7	503	13	B0106017
16	135.4	6.3	628	13	B0661641
17	131.8	6.1	748	28	BH590008
18	127	5.9	620	13	B0015066
19	127	5.9	644	28	BH646279
20	126.2	5.8	619	14	CA838661
21	125.6	5.8	461	13	B0104033
22	125	5.8	738	13	BQ914829
23	124.4	5.8	601	13	BQ862220
24	124	5.7	561	12	B1211954
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26	115	5.3	560	9	AL829373
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33	107.4	5.0	588	12	BJ247330
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37	105	4.9	669	13	BQ406738
38	101.6	4.7	734	28	BH528838
39	101.4	4.7	647	13	BQ403713
40	100.2	4.6	638	14	CA031253
41	99.2	4.6	649	13	BU000407
42	97.2	4.5	782	28	BH668366
43	96.4	4.5	700	9	AL506828
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45	92	4.3	393	9	AU225001

ALIGNMENTS

RESULT 1
BUS73954
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BUS73954 640 bp mRNA linear EST 17-SEP-2002
PA_Ea000SM16f Almond developing seed Prunus dulcis cDNA clone
BUS73954
BUS73954
EST.
BUS73954.1 GI:23032779
Prunus dulcis (almond)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Prunus dulcis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; rosids
; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
1 (bases 1 to 640)
Dandekar,A., Main,D., Wing,R. and Abbott,A.
Development of a Functional Genomics Database for Peach
Unpublished
Contact: Abbott, A.
Dept of Genetics and Biochemistry
Clemson University
122 Long Hall, Clemson University, Clemson, SC 29634, USA
Tel: 864 656 3060
Fax: 864 656 6879
Email: aalbert@clemson.edu
Total High Quality bases = 594
Seg primer: TAATACGCTCATCTATAGG
High quality sequence stop: 640.


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Db |||||
QY 1915 TACGAACCAACAGCCATCTTCAGGGCTTCTATCTGATG 1953
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QY 601 TACACACGAGGAGCCACCTTCAGGGCTTCTATCTGATG 639
Db |||||

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DEFINITION PA_Ea0009P08f, mRNA sequence.
ACCESSION BU575280
VERSION BU575280.1 GI:23034106
KEYWORDS EST.
SOURCE Prunus dulcis (almond)
ORGANISM Prunus dulcis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids 1; Rosales; Rosaceae; Amygdaloideae; Prunus.
1 (bases 1 to 654)
Dandekar,A., Main,D., Wing,R. and Abbott,A.
Development of a Functional Genomics Database for Peach
Unpublished
Contact: Abbott, A.
Dept of Genetics and Biochemistry
Clemson University
122 Long Hall, Clemson University, Clemson, SC 29634, USA
Tel: 864 656 3060
Fax: 864 656 6879
Email: aalbert@clemson.edu
Total High Quality bases = 597
Seq primer: TAATACGACTCACTATAGG
High quality sequence stop: 654.

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Db |||||
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QY 1298 AGCGAATCTTATGTTGGGAGTTTGTGTATGACATCTCTGTAATTTTCAATATT 1357
Db |||||
QY 206 TTTCCCATCTTACGTGGGAGTTTCTGATGACATCTCTGTAATTTTCAATATT 265
Db |||||
QY 1358 TGCCCCCAATCCAAATGAAGCCTCTCTGTAATTTTGTAGGATTTAGAGTGATTTATT 1417
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Db 266 TGCCCCCAATCCAAATGTAACCCACAAATTGTAATCTGTTCTAGGCATTTTCAAGATTTCT 325
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QY 626 TAGAAGTTTAAATTTTGGGAATCCCT 654
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RESULT 4
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LOCUS PA_Ea0007I08f Almond developing seed Prunus dulcis cDNA clone
DEFINITION PA_Ea0007I08f, mRNA sequence.
ACCESSION BU574474
VERSION BU574474.1 GI:23033299
KEYWORDS EST.
SOURCE Prunus dulcis (almond)
ORGANISM Prunus dulcis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids 1; Rosales; Rosaceae; Amygdaloideae; Prunus.
1 (bases 1 to 648)
Dandekar,A., Main,D., Wing,R. and Abbott,A.
Development of a Functional Genomics Database for Peach
Unpublished
Contact: Abbott, A.
Dept of Genetics and Biochemistry
Clemson University
122 Long Hall, Clemson University, Clemson, SC 29634, USA
Tel: 864 656 3060
Fax: 864 656 6879
Email: aalbert@clemson.edu
Total High Quality bases = 580
Seq primer: TAATACGACTCACTATAGG
High quality sequence stop: 648.

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synonym: Prunus amygdalus"
BASE COUNT 179 a 144 c 127 g 198 t

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Best Local Similarity 81.2%; Pred. No. 4.5e-77;
Matches 492; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

```


AUTHORS Dandekar, A., Main, D., Wing, R. and Abbott, A.
TITLE Development of a Functional Genomics Database for Peach
JOURNAL Unpublished
COMMENT Contact: Abbott, A.
 Dept of Genetics and Biochemistry
 Clemson University
 122 Long Hall, Clemson University, Clemson, SC 29634, USA
 Tel: 864 656 3060
 Fax: 864 656 6879
 Email: aalbert@clemson.edu

Total High Quality bases = 634
 Seq primer: TAATACGACTCACTATAGG
 High quality sequence stop: 658.

FEATURES

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 /tissue_type="embryo"
 /lab_host="E. coli"
 /clone_lib="Almond developing seed"
 /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI;
 synonym: Prunus amygdalus"
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Best Local Similarity 81.9%; Pred. No. 1.5e-70;
Matches 452; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

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 Db |||||
 QY 167 TTGTACGAGTAAGGGAGAGTATCGTAGTCAGGAGCAATTTGGAGCCCTCAATTC 226
 Db |||||
 QY 1238 TACTACTTAGTGGCGTGGACAGAGCTTACCTATCTCTCTCAACATCACAGTTGTC 1297
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 QY 227 TACTACTTAGCGGTGGGCGAGAGCTTACCTATCTCTCTAAATATCCAGTTGTC 286
 Db |||||
 QY 1298 AGCGAATCCTATGTTGGGAGTTCGTATGACATCTCTGTAATTCATTAATTT 1357
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 QY 287 TTTCCTATCTAGTCGGAGAGTTCGCAATGACATCTCTGTAATTCATTAACATTT 346
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 QY 407 ACCAATGTTCTTCTCGAGCTTGCCATTTACAACTCCACCTTCGTTTTTCCCTAGT 466
 Db |||||
 QY 1478 CATCTTACCCCTCCAAATTCGATTTTGTCTATATGTTAGCAAGTTCCAGGCAT 1537
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 QY 467 CATCTTATCCCTCCAAATTCGATTTTGTCTATATGTTAGCAAGTTCCAGGCAT 526
 Db |||||
 QY 1538 TGTCTCATGTTTCTGTGACGTAATTCATCTGACGTGAGATCTGCTCCAAATTTA 1597
 Db |||||
 QY 527 TATCATATGTTTCTCTACACTGAATCACTCTCAATGTGAGAGTCAGTCCAAATGTC 586
 Db |||||
 QY 1598 AATTCAATTAATTCAAATTCACAGACCTTGTCTAAATGTTAGCGGCATGAAGAGC 1657
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 QY 587 AATTAATTAATTCAAATTCGACAGATCTTCTCTATGTTGTTAGCGGCATGAAGAG 646
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RESULTS

BU645516 598 bp mRNA linear EST 01-MAY-2003
LOCUS EST989 almond cDNA library Prunus dulcis cDNA 5', similar to
DEFINITION mandelonitrile lyase, mRNA sequence.
 BU645516 GI:30271383
VERSION BU645516.1
KEYWORDS EST.
SOURCE Prunus dulcis (almond)
ORGANISM Prunus dulcis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 / eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
 1 (bases 1 to 598)
REFERENCE Jiang, Y.Q. and Ma, R.C.
AUTHORS Generation and Analysis of Expressed Sequence Tags from Almond
TITLE (Prunus dulcis) Pistils
JOURNAL Unpublished
COMMENT Contact: Jiang YQ, Ma RC
 Lab of Plant Functional Genomics
 Beijing Agro-biotechnology Research Center
 Beijing Cun, No.301, Haidian Dis., Beijing 100089, P.R. China
 Tel: 8610 5150 3831
 Fax: 8610 5150 3980
 Email: rcma@yahoo.com
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 Seq primer: M13/pUC reverse primer
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FEATURES

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 using oligo(dT) cellulose as described. cDNA was
 synthesized using a lambda-ziplox cDNA synthesis kit (CAT
 No.19643-014, Invitrogen, USA). The phage library was
 converted through mass excision to a plasmid library in
 the vector pZLI. The plasmid library was plated on 15-cm
 LB agar plates with 100ug/mL ampicillin. Individual clones
 were picked at random and propagated. The 5' ends of the
 cDNA clones were sequenced on ABI Prism377 DNA sequencer."
 168 a 122 c 133 g 175 t

BASE COUNT

ORIGIN
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 Best Local Similarity 74.5%; Pred. No. 9e-69;
 Matches 537; Conservative 0; Mismatches 1; Indels 203; Gaps 1;
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 Db 1 AACATTTCATCTATAGTCACACAGCAATGATGGACCTGATTCGTCAATAGACA 60
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 QY 707 ATAGAGAGGAGGATTCCTGAGCGGATTCCTTCAGCAATATCAATCTTGGCAATCTGT 766
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QY 887 GAGAGATCCTCTCTCTCCAAATACATCAAGTATGTCATCAGTCAATTAATGGA 946
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RESULT 8
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 DEFINITION PA_Ea0001J20f, mRNA sequence.
 ACCESSION BUS72692
 VERSION BUS72692.1 GI:23030899
 KEYWORDS EST.
 SOURCE Prunus dulcis (almond)
 ORGANISM Prunus dulcis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
 1 (bases 1 to 556)
 Dandekar,A., Main,D., Wing,R. and Abbott,A.
 Development of a Functional Genomics Database for Peach
 Unpublished
 Contact: Abbott, A.
 Dept of Genetics and Biochemistry
 Clemson University
 122 Long Hall, Clemson University, Clemson, SC 29634, USA
 Tel: 864 656 3060
 Fax: 864 656 6879
 Email: aalbert@clemson.edu
 Total High Quality bases = 560
 Seq primer: TAATACGACTCACTATAGG
 High quality sequence stop: 656.
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 /clone="PA_Ea0001J20f"
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/clone lib="Almond developing seed"
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 synonym: Prunus amygdalus"
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 Best Local Similarity 75.4%; Pred. No. 3.4e-67;
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 QY 1500 GACTTTTGTCTATTTAGTCCAAAGTTCCAGGACATTTCTCATGTTCTGTCAAGCT 1559
 Db 62 GACTTTTGTCTACTTTGTAGCAAGTGGCAGACCTTATCTTATGTTCTCTCACACT 121
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 QY 1680 GGCATTAGAACCATATAAGCTCGAGATGTGCTGGGAATTTGACGTTTCAATTTATTTGGG 1739
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 QY 1800 TGTAGCTTCATAGTGGCATTCACCGTGGGAAGCCCTTGTGGGAAGTGTCTTGATGACAG 1859
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 Db 602 CTTTGTTTTAAACTTGA 620

RESULT 9
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 LOCUS PA_Ea0008H17f Almond developing seed Prunus dulcis cDNA clone
 DEFINITION PA_Ea0008H17f, mRNA sequence.
 ACCESSION BUS74792
 VERSION BUS74792.1 GI:23033617
 KEYWORDS EST.
 SOURCE Prunus dulcis (almond)
 ORGANISM Prunus dulcis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
 1 (bases 1 to 634)
 Dandekar,A., Main,D., Wing,R. and Abbott,A.
 Development of a Functional Genomics Database for Peach
 Unpublished
 Contact: Abbott, A.

Dept of Genetics and Biochemistry
Clemson University
122 Long Hall, Clemson University, Clemson, SC 29634, USA
Tel: 864 656 3060
Fax: 864 656 6879
Email: aalbert@clemson.edu
Total High Quality bases = 573
Seq primer: TAATACGACTCATTATAGG
High quality sequence stop: 634.

FEATURES

source

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/clone_lib="Almond developing seed"
/notes="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI;
synonym: Prunus amygdalus"
174 a 154 c 111 g 194 t 1 others

BASE COUNT 174 a 154 c 111 g 194 t 1 others

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Matches 411; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

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DB 192 TTGTACGCGCAGTAGGAGAGTTATCGTGTGAGGCAATTCGGAACGCTCAGCTTC 251
QY 1238 TACTACTTGTGCGGTGTGACAGAGTCTTACCTATCTCTCTACATCAGAGTTGTC 1297
DB 252 TACTACTTGTGCGGTGTGACAGAGTCTTACCTATCTCTCTACATCAGAGTTGTC 311
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DB 432 ACCAAGTTTCTGTGCAAGCTTCCCAATTTTCCACTCCACCTTTAGTCTTTTCCACAA 491
QY 1478 CATCTTACCCCTCCCAATTCGACTTTTGTCTCATATTTGTAGCCAAAGTTCCAGGACCAT 1537
DB 492 CATCTTACCCCTCCCAATTCGACTTTTGTCTCATATTTGTAGCCAAAGTTCCAGGACCAT 551
QY 1538 TGCTCATGTTCTGTGCAAGCTTCCCAATTTTCCACTCCACCTTTAGTCTTTTCCACAA 1597
DB 552 TATCTTATGTTCTGTGCAAGCTTCCCAATTTTCCACTCCACCTTTAGTCTTTTCCACAA 611
QY 1598 AATTCATTTACTATTTCAAT 1617
DB 612 AATTCATTTACTATTTCAAT 631

RESULT 10
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LOCUS BU574699
DEFINITION PA_Ea0008D07f Almond developing seed Prunus dulcis cDNA clone
ACCESSION BU574699
VERSION BU574699.1 GI:23033524
KEYWORDS EST.

SOURCE

ORGANISM

Prunus dulcis (almond)

Prunus dulcis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; euroside 1; Rosales; Rosaceae; Amygdaloideae; Prunus.

1 (bases 1 to 626)

Dandekar, A., Main, D., Wing, R. and Abbott, A.

Development of a Functional Genomics Database for Peach

Unpublished

Contact: Abbott, A.

Dept of Genetics and Biochemistry

Clemson University

122 Long Hall, Clemson University, Clemson, SC 29634, USA

Tel: 864 656 3060

Fax: 864 656 6879

Email: aalbert@clemson.edu

Total High Quality bases = 576

Seq primer: TAATACGACTCATTATAGG

High quality sequence stop: 626.

FEATURES

source

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/clone_lib="Almond developing seed"
/notes="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI;
synonym: Prunus amygdalus"
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BASE COUNT

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Best Local Similarity 85.9%; Pred. No. 4.4e-55;
Matches 352; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

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DB 84 AGCATTAATCAATGAGCGCTCTAGCCAGAGCTAACATTTTCATCTATAGTCAACAGGA 143
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DB 144 GTTGATTGGACATGGAATTCGTTAATCAGACATATAGTGGTGAAGACCATTTGTG 203
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QY 734 ATTCTTCAGACAATGGAATTTAGTTTGATCAGCAGCAGCACTAGACTCACCGGCTCA 793
DB 264 GTTCATCAAAACCATGGAATTTAGTTTAGATCATGAAGAGGATAGTAATTTACCGGCTCA 323
QY 794 ACTTTTGACAATTAATGAACGCGACATCGGCTGATGAACCTGCTTAATAAAGGAGACCT 853
DB 324 ACTTTTGACAACAGGGAACGAGACATGACCTGATGAACCTTCTTAATAAAGGAACTCT 383
QY 854 AATACTTGTGATGTTGAGTTTCAGGCTTCAGTAGAGAGATCTCTTCTTC 903
DB 384 AACACTTGGAGTTGAGTTTCAGGCTTCAGTAGAGAGATCTCTTCTTC 433

RESULT 11
BU574357 505 bp mRNA linear EST 17-SEP-2002
LOCUS BU574357
DEFINITION PA_Ea0007C13f Almond developing seed Prunus dulcis cDNA clone
ACCESSION BU574357
VERSION BU574357
KEYWORDS EST.

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VERSION      BU574357.1  GI:23033182
SOURCE       EST.
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ORGANISM     Prunus dulcis
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             Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
             ; eurosids 1; Rosales; Rosaceae; Amygdaloideae; Prunus.
REFERENCE    Dandekar,A., Main,D., Wing,R. and Abbott,A.
AUTHORS      Development of a Functional Genomics Database for Peach
TITLE        Unpublished
JOURNAL      Contact: Abbott, A.
COMMENT      Dept of Genetics and Biochemistry
             Clemson University
             122 Long Hall, Clemson University, Clemson, SC 29634, USA
             Tel: 864 656 3060
             Fax: 864 656 6879
             Email: aalbert@clemson.edu
             Total High Quality bases = 255
             Seq primer: TAATACGACTCACTATAGG
             High quality sequence stop: 505.
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             /tissue_type="embryo"
             /lab_host="E. coli"
             /clone_lib="Almond developing seed"
             /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI;
             synonym: Prunus amygdalus"
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Best Local Similarity 77.7%; Pred. No. 1.3e-54;
Matches 393; Conservative 0; Mismatches 112; Indels 1; Gaps 1;

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QY 368 TTATCAGAAAATACAAAGTGTCTTCTTAGAAGAGGCACTATCTCTACAGAAATACCCG 427
Db 61 TTATCAGAAAATACAAAGTGTCTTCTTAGAAGAGGCACTATCTCTCGACAGCATATCC 119
QY 428 AACACGTTGACTGCAGATGGTTTGCATATATCTCGACCAACAGATGATGGAAGACG 487
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QY 488 CCAGTTGAAAGTTGCTGTCGGAAGATGGCATATGATAATGTGCGAGCCAGATCCTCGGT 547
Db 180 CCGTGCAGAAAGTTGGTGTCCGAGATGGTATTGATPAATGATACGGGACGGTGTCTGT 239
QY 548 GGCACGACCATATCAATGACGGGTCTACGCGAGAGCTAACATTCATTTCTATATGCAA 607
Db 240 GGCACAGCATATCAATGCGGTGTCTAGCCCAACACCTAACACCTCAATCTATAGTGA 299
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QY 668 ATTGTGGTCAAGCCAAATATCAATCTTGGCAATCTGTTATAGAGAGGATTTCTTGGAG 727
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QY 728 GCGGGTATCTTTCAGCAATATGATTTAGTTTGTGATCAGGAACAGCAATAGACTCACC 787
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QY 788 GGCTCAACTTTTGACATAATGGNAC 813

Db 480 TGCTCATCTCTTTTAACAGCCAGGTAC 505
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DEFINITION PA_Ea0007001f Almond developing seed Prunus dulcis cDNA clone
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ACCESSION BU574592
VERSION   BU574592.1 GI:23033417
KEYWORDS  EST.
SOURCE    Prunus dulcis (almond)
ORGANISM  Prunus dulcis
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            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
            ; eurosids 1; Rosales; Rosaceae; Amygdaloideae; Prunus.
REFERENCE  1 (bases 1 to 621)
AUTHORS    Dandekar,A., Main,D., Wing,R. and Abbott,A.
TITLE      Development of a Functional Genomics Database for Peach
JOURNAL    Unpublished
COMMENT    Contact: Abbott, A.
            Dept of Genetics and Biochemistry
            Clemson University
            122 Long Hall, Clemson University, Clemson, SC 29634, USA
            Tel: 864 656 3060
            Fax: 864 656 6879
            Email: aalbert@clemson.edu
            Total High Quality bases = 591
            Seq primer: TAATACGACTCACTATAGG
            High quality sequence stop: 621.
            Location/Qualifiers
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Best Local Similarity 84.7%; Pred. No. 1.2e-39;
Matches 272; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 289 CACTGATACAGCTCGGAAGGATCATATGACTATGATCGGTGAGGAAATCAGG 348
Db 2 CACTGATCTAGAGTTGGAAGGATCATATGACTATGATCGGTGAGGAAATCAGG 61
QY 349 GGTCCATTGCGCAGCACTTTATCAGAAATACAGGTGCTTCTTCTAGAAAGGCAC 408
Db 62 GTGTCCATTGCGCAGCACTTTATCAGAAATACAGGTGCTTCTTCTGAAAGGGCAG 121
QY 409 TATTCTCTACAGAAATACCCGAAACAGCTTGACTGACATGGGTTCGATATAATCTGACGA 468
Db 122 TCTTCGACAGCATATCCCAAGTCTTGACTGAGATGGGTTCGATATAATCTCCAGCA 181
QY 469 ACAAGATGATGGAAGAGCCGAGTTGAAGTTTCGTGTCGAAAGATGCAATGATGTAATGT 528
Db 182 AGAAGATGATGGAAGAGCACCGGTGCGAAAGTTTCGTGTCGAAAGATGTAATGTAATGT 241
QY 529 GCGAGCCAGGATCTTCGGTGGCAGCACCATATCAATGACAGCCCTCTACGCGAGCTAA 588
Db 242 ACGGGGCGAGGGTGTCTCGGTGGCAGCAAGCATGATCAATGCGGTGTCTTACGCGAGCCAA 301
QY 589 CATTTTCATTCTATAGTCAAAAC 609
Db 302 CACCTCAATCTATAGTGCATC 322

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RESULT 13
BUS74379
LOCUS
DEFINITION
    PA_Ea0007D17f Almond developing seed Prunus dulcis cDNA clone
ACCESSION
    BUS74379
VERSION
    BUS74379.1 GI:23033204
KEYWORDS
    EST.
SOURCE
    Prunus dulcis (almond)
ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
    i; eurosids 1; Rosales; Rosaceae; Amygdaloideae; Prunus.
REFERENCE
    1 (bases 1 to 622)
AUTHORS
    Dandekar,A., Main,D., Wing,R. and Abbott,A.
TITLE
    Development of a Functional Genomics Database for Peach
JOURNAL
    Unpublished
COMMENT
    Contact: Abbott, A.
    Dept of Genetics and Biochemistry
    Clemson University
    122 Long Hall, Clemson University, Clemson, SC 29634, USA
    Tel: 864 656 3060
    Fax: 864 656 6879
    Email: aalbert@clemson.edu
    Total High Quality bases = 600
    Seq primer: TAATACGACTCACTATAGG
    High quality sequence stop: 622.
    Location/Qualifiers
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            /organism="Prunus dulcis"
            /mol_type="mRNA"
            /cultivar="Nonpareil"
            /db_xref="taxon:3755"
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            /tissue_type="embryo"
            /lab_host="E. coli"
            /clone_lib="Almond developing seed"
            /notes="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI;
            synonym: Prunus amygdalus"
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    Best Local Similarity 84.7%; Pred. No. 1.2e-39;
    Matches 272; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY    289  CACTGATACAGCTCGGAAGATCATATGACTACATTTGTAATCGTGGAGGACATCNGG 348
Db    2   CACTGATCTAGCTTGGAGAGATCATATGACTATGTTATGTTGGCGGAGGACATCAGG 61

QY    349  GTGTCCATTTGGACAACTTTATCAGAAAAATACAGGTGCTTCTTCTAGAAAGAGGCAC 408
Db    62  GTGTCCATTTGGACAACTTTATCAGAAAAATACAGGTGCTTCTTCTAGAAAGAGGCAC 408

QY    409  TATTGCTACAGATACCGACAGCTTGACTGACGAGTGGTTGTCATATATCTGACGCA 468
Db    122  TCITCCGACAGCATATCCCAACGCTTGTGCTGACAGATGGTTGTATATATCTCCAGCA 181

QY    469  ACAAGATGATGGAAGAGCGGCAGTTGAAAGCTTGTCTCCGAGATGGCATATGATGT 528
Db    182  AGAAGATGATGGAAGAGCACCGGTGCAAGAGTTGTGTCTCCGAGATGGTATGATATGT 241

QY    529  GCGAGCAGGATCTCGGTGGCAGCACCAATCAATGCAAGGCTGTACCCAGAGCTAA 588
Db    242  ACGGGGAGGCTGCTGGTGGCAGCATGATCCCGGTGTCTACCCAGAGCCAA 301

QY    589  CATTTCATTCTATAGTCAAC 609
Db    302  CACCTCAATCTATAGTCATC 322

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RESULT 14
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LOCUS
DEFINITION
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ACCESSION
    BUS72781
VERSION
    BUS72781.1 GI:23031361
KEYWORDS
    EST.
SOURCE
    Prunus dulcis (almond)
ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
    i; eurosids 1; Rosales; Rosaceae; Amygdaloideae; Prunus.
REFERENCE
    1 (bases 1 to 543)
AUTHORS
    Dandekar,A., Main,D., Wing,R. and Abbott,A.
TITLE
    Development of a Functional Genomics Database for Peach
JOURNAL
    Unpublished
COMMENT
    Contact: Abbott, A.
    Dept of Genetics and Biochemistry
    Clemson University
    122 Long Hall, Clemson University, Clemson, SC 29634, USA
    Tel: 864 656 3060
    Fax: 864 656 6879
    Email: aalbert@clemson.edu
    Total High Quality bases = 531
    Seq primer: TAATACGACTCACTATAGG
    High quality sequence stop: 543.
    Location/Qualifiers
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            /cultivar="Nonpareil"
            /db_xref="taxon:3755"
            /clone="PA_Ea0001014f"
            /tissue_type="embryo"
            /lab_host="E. coli"
            /clone_lib="Almond developing seed"
            /notes="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI;
            synonym: Prunus amygdalus"
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    Best Local Similarity 71.7%; Pred. No. 7.6e-28;
    Matches 243; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY    1720  GACGGTTTCAATATTGGGAGTACCTTTGCCAGAGACCAACAGATGATGATCCTTC 1779
Db    3   GAAGGTTTTAATATTGGGAATCCCTTTGCCAAGGACCAACAGATGATGATCCTTC 62

QY    1780  GAAACATTTTGTCTAGATAATGTAGCTTCATATCTGGCATTCACCGGTGGAGCCTTGT 1839
Db    63  GAAACATTTTGGCGAGATCAGTAGSCTCATATGGCACTACCAAGGTGGATGCTTGT 122

QY    1840  GGGAAAGCTCTTGATGACAGTTTCGCTGTATGGGGATCAAAGCATACGGCTTTGAT 1899
Db    123  GGGAAAGGCTCTTGATGAGTTTTCGTTGTACAGGGATCAATGATACGGCTTTGAT 182

QY    1900  GCTCCACTTCCCTTAGCAACCAACAGCCATCCTCAGGGCTTCTATCATGATTTAGGA 1959
Db    183  GCTCAACATTTCCCTTACACACAGCCATCCTCAGGGCTTCTATCATGATTTAGGG 242

QY    1960  AGGTATGATGATGCACACTTCCAAACCATAGAGATTCATATATTTGTTGTTGAT 2019
Db    243  AGGTATGATGATGATTAATTCCTCAAGAGATGATTCAGATCTAAATCTTGAT 302

QY    2020  GAATCTCTGCGGATGCTCTCTTTTATTAATCTTAA 2058
Db    303  TCCCTCAAGTCAGCAGCATCCTTTGTTTAAACTGA 341

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RESULT 15
BQ106017

LOCUS	503 bp	mRNA	linear	EST 16-APR-2002
DEFINITION	fc1266.e Rose Petals (Fragrant Cloud) Lambda Zap Express Library			
ACCESSION	B0106017	Rosa hybrid cultivar cDNA clone fc1266.e 5', mRNA sequence.		
VERSION	B0106017.1	GI:20155679		
KEYWORDS	EST.			
SOURCE	Rosa hybrid cultivar			
ORGANISM	Rosa hybrid cultivar			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids			
AUTHORS	1. (bases 1 to 503)			
	Guterman,I., Shalit,M., Menda,N., Piestun,D., Dafny-Yelin,M., Shalev,G., Bar,E., Davydov,O., Ovadis,M., Emanuel,M., Wang,J., Adam,Z., Pichersky,E., Lewinsohn,E., Zamir,D., Vainstein,A. and Weiss,D.			
TITLE	Rose Scent: Genomics Approach to Discovering Novel Floral Fragrance-Related Genes			
JOURNAL	Plant Cell 14 (10), 2325-2338 (2002)			
COMMENT	Contact: Naama Menda Petal Genomics Faculty of Agricultural, Food and Environmental Quality Sciences, The Hebrew University of Jerusalem P.O. Box 12, Rehovot, 76100, Israel Tel: 972 8 9489 389 Fax: 972 8 9468 263 Email: shaham@agri.huji.ac.il Seq primer: T3 forward. Location/Qualifiers 1..503 /organism="Rosa hybrid cultivar" /mol_type="mRNA" /strain="Fragrant Cloud" /db_xref="taxon:128735" /clone="fc1266.e" /tissue_type="Petals" /dev_stage="Young open flower at stage four" /clone_l1b="Rose Petals (Fragrant Cloud) Lambda Zap Express Library" /notes="Vector: pBKMV; Site1: EcoRI; Site_2: XhoI"			
BASE COUNT	131 a	98 c	127 g	147 t
ORIGIN				
Query Match	6.7%	Score 143.8	DB 13	Length 503
Best Local Similarity	77.1%	Pred. No. 3e-19		
Matches 175	Conservative	0	Mismatches 52	Indels 0
Gaps	0			
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Db	277	CAGGTGTTTCGGCTCGAGGGGTGTATATATTGATTCTAATGGAGTCTCATCGGCAT	336	
QY	1178	TTGTACGCGTACGCGAGAGTTATGTTAGTCGCGGACAAATCGAACGCTCAGCTTC	1237	
Db	337	TTGTACGTGTAGGAGAGGATTATTCGTAGTCGAGGGCAATTTGGAGTCTCTCAGCTTC	396	
QY	1238	TACTACTTAGTGGCGTTGGACACGAGTCTTACCTATCTTCTCTCAACATCACAGTTGTTTC	1297	
Db	397	TACTTCTTAGCGGTGTTGGTCTCTCAGTCCTATCTATCATCTTTCAAAATCCCAAGTTGTTTC	456	
QY	1298	ACCGCAATCCTATGTTGGCGAGTGTGTGTATGACAAATCCTCGTAAT	1344	
Db	457	ACCCCCAACTCACACTCGAAACTTTATGTATGACAAATCCTCGTAAT	503	

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Job time : 4540 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2003, 15:05:47 : Search time 575 Seconds
(without alignments)
10149.887 Million cell updates/sec

Title: US-10-046-232-19

Perfect score: 2162

Sequence: 1 ggaattcacaataggagaa.....agtcacatgtgaagaattccg 2162

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_19Jun03.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2162	100.0	2162	24	AAF88778
2	1272	58.8	1632	24	AAF88779
3	1202.4	55.6	2087	24	AAF88780
4	138	6.4	2017	21	AAC50945
5	138	6.4	2104	21	AAC50934
6	129.4	6.0	1854	24	AB214369
7	123.4	5.7	1837	21	AAC39108
8	122.4	5.7	2098	21	AAC40757

9	68	3.1	68	24	AAF88763	Almond HNL5 PCR pr
c 10	65	3.0	73	24	AAF88768	Almond HNL5 PCR pr
c 11	60.6	2.8	925	24	AAF98636	Arabidopsis thalia
12	59.4	2.7	300	24	ABL73822	Corn tassell-derive
13	59.2	2.7	645	22	AH87692	Peppermint plant o
14	58.6	2.7	276	24	ABL72070	Corn tassell-derive
15	55.2	2.6	978	21	AAC40702	Arabidopsis thalia
c 16	54.6	2.5	441	24	ABL94144	Arabidopsis thalia
17	51.2	2.4	267	25	ABX18148	Human GDP-mannose
18	49	2.3	64	24	AAF88762	Almond HNL5 PCR pr
19	48.8	2.3	693	21	AAC44595	Arabidopsis thalia
c 20	46.6	2.2	66	24	AAF88767	Arabidopsis thalia
21	46.2	2.1	6641	24	ABL54335	Chemically treated
22	46.2	2.1	6641	24	ABL32314	Human immune syste
23	45.4	2.1	114	24	AAF88769	Human immune syste
24	45	2.1	1863	21	AAA15501	Almond HNL5 PCR pr
25	45	2.1	1863	22	AAC83943	Fusarium venenatum
26	45	2.1	1863	24	ABA91281	Choline oxidase co
27	45	2.1	55008	22	AAK80495	Fusarium venenatum
c 28	44.6	2.1	1470	15	AAQ55185	Human immune/haema
29	43.4	2.0	37973	24	ABL34196	MS-lei610 Vector.
c 30	42.8	2.0	7607	24	ABL34196	Human immune syste
31	41.2	1.9	1595	22	AAU00325	Human metastasis a
c 32	41.2	1.9	3744	21	AAAT70149	Human reproductiv
c 33	41	1.9	6056	24	ABL33027	Plasmodium falcipa
c 34	41	1.9	9268	24	ABL33600	Human immune syste
c 35	40.6	1.9	8759	25	ABZ09964	Human immune syste
c 36	40.6	1.9	8759	25	ABZ10092	Haematopoietic cel
c 37	40.6	1.9	8759	25	ABZ10110	Haematopoietic cel
c 38	40.6	1.9	8759	25	ABZ10238	Haematopoietic cel
c 39	40.6	1.9	16236	24	ABL33022	Haematopoietic cel
c 40	40.4	1.9	8056	25	ABZ10246	Haematopoietic cel
c 41	40	1.9	160	21	AAC25257	Human immune syste
c 42	40	1.9	2527	24	ABK35091	Human secreted pro
c 43	40	1.9	4043	24	ABX91986	Human cDNA encodin
c 44	40	1.9	6527	18	AA760141	Lung specific nucl
c 45	40	1.9	16811	24	ABL33946	Antirrhinum centro

ALIGNMENTS

RESULT 1

AAF88778

ID AAF88778 standard; DNA; 2162 BP.

XX AC

AAF88778;

11-DEC-2002 (first entry)

XX AC

Almond mdl5 and MDL1 homologue DNA SEQ ID 19.

DE DE

Almond; hydroxynitrile lyase; HNL; (R)-cyanohydrin synthesis; vitamin;

KW KW

(S)-cyanohydrin synthesis; pyrethroid; gene; ds.

XX XX

Prunus amygdalus.

OS OS

Prunus amygdalus.

XX XX

Key	Location/Qualifiers
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FT FT	13..115
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FT FT	/number= 1
FT FT	116..257
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FT FT	/number= 1
FT FT	258..917
FT FT	/*tag= d
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FT FT	918..1120
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ALIGNMENTS

RESULT 1	AAF88778	standard; DNA; 2162 BP.
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XX	AC	
DT	11-DEC-2002	(first entry)
XX	Almond mdl5 and MDL1 homologue DNA SEQ ID 19.	
XX	Almond; hydroxynitrile lyase; HNL; (R)-cyanohydrin synthesis; vitamin;	
KW	(S)-cyanohydrin synthesis; pyrethroid; gene; ds.	
XX	Prunus amygdalus.	
OS	Prunus amygdalus.	
XX	Key	Location/Qualifiers
FT	CDS	13..2153
FT		/tag= a
FT		/product= "MDL-homologue"
FT		/note= "This coding sequence is interrupted by introns"
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FT	intron	116..257
FT		/tag= c
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FT	exon	258..917
FT		/tag= d
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 PF 18-DEC-2001; 2001EP-0130058.
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 PA (STAM) DSM FINE CHEM AUSTRIA NFG GMBH & CO KG.
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 XX Schwab H, Glieder A, Kratky C, Dreveny I, Poeschlauer P, Skranc W;
 PI Mayrhofer H, Wirth I, Neuhofer R, Bona R;
 XX
 DR WPI; 2002-645687/70.
 DR P-PSDB; AAB71494.
 XX
 New gene for hydroxynitrile lyase from Prunus species, useful for
 stereospecific synthesis of cyanohydrin -
 Claim 3; Fig 1; 49pp; German.
 XX
 CC This invention describes a novel gene that encodes a hydroxynitrile lyase
 CC (HNL) isolated using one PCR primer based on the 5'-region of the mdl
 CC gene of Prunus serotina or P. amygdalus and a second PCR primer, based on
 CC the 3'-region of an HNL isoenzyme from the same species. The signal
 CC region of the HNL protein can be used for secretory expression of
 CC heterologous proteins, e.g. fusion proteins, with HNL activity in host
 CC cells. The products of the invention are useful for synthesis of (R)- or
 CC (S)-cyanohydrins, e.g. for synthesis of pharmaceuticals, vitamins and
 CC pyrethroids. Recombinant expression of HNL produces technically useful
 CC amounts of HNL, and these allow stereoselective synthesis of both (R)-
 CC or (S)-cyanohydrins. This sequence encodes a protein homologue of
 CC Prunus serotina mdl5 gene and the Prunus amygdala MDL1 gene described in
 CC the method of the invention.
 XX
 SQ Sequence 2162 BP; 619 A; 437 C; 428 G; 678 T; 0 other;
 Query Match 100.0%; Score 2162; DB 24; Length 2162;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGAATTCAATATGGAGAAATCAACAATGTCAGTTATACATATTGGTGGCATCTTCT 60
 DB 1 GGAATTCAATATGGAGAAATCAACAATGTCAGTTATACATATTGGTGGCATCTTCT 60
 QY 61 GTTCTTCATCTTCAGTATTCAGAGGTTCACTCGCTTGGCCAAATCTTCTCATGGTAA 120
 DB 61 GTTCTTCATCTTCAGTATTCAGAGGTTCACTCGCTTGGCCAAATCTTCTCATGGTAA 120
 QY 121 TTTCATCTTCAGTATTCATTAACACGAAATGTCAGTATTAATTAATTAAGAAACTGA 180
 DB 121 TTTCATCTTCAGTATTCATTAACACGAAATGTCAGTATTAATTAATTAAGAAACTGA 180
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QY 301 CTCGGAAGGATCATATGACTACATTTGTAATCGGTGGAGGAAACATCAGGGTGTCCATTGGC 360
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 QY 361 AGCAACTTTATCAGAAAAATCAAGGTGCTTCTTAGAAGAGGACACTATTGCTACAGA 420
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 QY 481 AAAGACGCGAGTTGAAAGGTTCTGTCGGAAGATGGCATTTGATATGTCGAGCCAGGAT 540
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 QY 481 AAAGACGCGAGTTGAAAGGTTCTGTCGGAAGATGGCATTTGATATGTCGAGCCAGGAT 540
 DB |||||
 QY 541 CCTCGGTGGCAGCACCATTAATCAATGCGAGGGTCTACGCCAGAGCTAATCTTCAATTT 600
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 QY 601 TAGTCAACACAGGAATTTGAATGGACCTGGATTTGGTCAATTAAGACATATGAGTGGTTGA 660
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 DB |||||
 QY 661 AGACGCCATTTGTTGTCAGGCCAAATCAATCAATCTTTGGCAATCTGTTATAGGAGGGATT 720
 DB |||||
 QY 721 CTTGAGAGCGGGTATTTCTTCCAGCAATGGATTTAGTTTGGATCAGGAGCAGGACTAG 780
 DB |||||
 QY 721 CTTGAGAGCGGGTATTTCTTCCAGCAATGGATTTAGTTTGGATCAGGAGCAGGACTAG 780
 DB |||||
 QY 781 ACTCACCGGCTCAACTTTTGGCAATTAATGGAACCGCACATCGGCTGATGAATGCTTAA 840
 DB |||||
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 QY 841 TAAAGAGACCCCTAATAACTTTGCTAGTTGCGAGTTCCAGGCTCAGTAGAAGAGATCTCTT 900
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 QY 1081 GTTTAGTTTGACAAATAATTAAGCTATTTCTTAATGCAGATTTTGTACAGTATTGGAGTC 1140
 DB |||||
 QY 1081 GTTTAGTTTGACAAATAATTAAGCTATTTCTTAATGCAGATTTTGTACAGTATTGGAGTC 1140
 DB |||||
 QY 1141 ATATATACGGATTCGATGGAACCTCTCATCAGGCAATTTGACGGGTAAACGGAGAAGTT 1200
 DB |||||
 QY 1141 ATATATACGGATTCGATGGAACCTCTCATCAGGCAATTTGACGGGTAAACGGAGAAGTT 1200
 DB |||||
 QY 1201 ATTGTTAGTGCAGGACATCGGAACCGCTCAGCTTCTACTACTAGTGGGTTGGACCA 1260
 DB |||||
 QY 1201 ATTGTTAGTGCAGGACATCGGAACCGCTCAGCTTCTACTACTAGTGGGTTGGACCA 1260
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 QY 1261 GAGCTTACCTATCTTCTCAACATCACAGTGTCTCAGCCGAATCTTATGTTGGGCG 1320
 DB |||||
 QY 1261 GAGCTTACCTATCTTCTCAACATCACAGTGTCTCAGCCGAATCTTATGTTGGGCG 1320
 DB |||||
 QY 1321 TTTGTTATGACAAATCTCTGTAATTTTCAATTAATTTTGGCCCCCAATCCCAATTTGAAGCC 1380
 DB |||||
 QY 1321 TTTGTTATGACAAATCTCTGTAATTTTCAATTAATTTTGGCCCCCAATCCCAATTTGAAGCC 1380
 DB |||||
 QY 1381 TCTGTTGTAACCTGTTTGGCAATTAGAGGATTTATTAACAAGTTTCTCTGTCAAGCTTG 1440


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Db 1381 TCTGTTGTAACCTGTTTGGCAATAGAGTCAATATATATCAGTTTCTGTGCAAGCTTG 1440
QY 1441 CCAATTTCCACTCCACCCTTTAGTCTTTTCTTCCCTCAACATCTTACCCTCCCAAAATCG 1500
Db 1441 CCAATTTCCACTCCACCCTTTAGTCTTTTCTTCCCTCAACATCTTACCCTCCCAAAATCG 1500
QY 1501 ACTTTTGTCTCATATTTGTTAGCCAAAGTCTCCAGGACCATGCTCATGTTCTGTGACGCTA 1560
Db 1501 ACTTTTGTCTCATATTTGTTAGCCAAAGTCTCCAGGACCATGCTCATGTTCTGTGACGCTA 1560
QY 1561 AATTCAATCATCTGACGTGAGAAATCGCTCCAAATTAATAATCAATTAATTAATTAATTC 1620
Db 1561 AATTCAATCATCTGACGTGAGAAATCGCTCCAAATTAATAATCAATTAATTAATTAATTC 1620
QY 1621 ACAGACCTTGTCTAATTTGTTAGCCAAAGTCTCCAGGACCATGCTCATGTTCTGTGACGCTA 1680
Db 1621 ACAGACCTTGTCTAATTTGTTAGCCAAAGTCTCCAGGACCATGCTCATGTTCTGTGACGCTA 1680
QY 1681 GCATTAGAACCATATAAAGCTCGAGATGCTGCGGAATTCAGCGTTTCAATTTATTTGGGA 1740
Db 1681 GCATTAGAACCATATAAAGCTCGAGATGCTGCGGAATTCAGCGTTTCAATTTATTTGGGA 1740
QY 1741 GTACCTTTGCCAGAGAACCAACAGATGATGATCCTTCGAAACATTTTGTCTAGATAAT 1800
Db 1741 GTACCTTTGCCAGAGAACCAACAGATGATGATCCTTCGAAACATTTTGTCTAGATAAT 1800
QY 1801 GTAGCTTCATCTGCGATACCAAGTGGAGCCCTTGTGGAAAGTGTGATGACAGT 1860
Db 1801 GTAGCTTCATCTGCGATACCAAGTGGAGCCCTTGTGGAAAGTGTGATGACAGT 1860
QY 1861 TTCCGTTGTATGGGATCAAGCATTAACGGTGTGATGATGATGATGATGATGATGATGATGAT 1920
Db 1861 TTCCGTTGTATGGGATCAAGCATTAACGGTGTGATGATGATGATGATGATGATGATGATGAT 1920
QY 1921 CCAACAGCCATCTCAGGCTTCTATCTGATGTTAGGAGGTATGATGATGATGATGATGATGAT 1980
Db 1921 CCAACAGCCATCTCAGGCTTCTATCTGATGTTAGGAGGTATGATGATGATGATGATGATGAT 1980
QY 1981 AACCACTAGATGATCTCAATATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2040
Db 1981 AACCACTAGATGATCTCAATATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2040
QY 2041 TTTTATTAATCTTAAATTTTGTGTTTGGCAGGTATGTTGGGCTTCAATCTCTG 2100
Db 2041 TTTTATTAATCTTAAATTTTGTGTTTGGCAGGTATGTTGGGCTTCAATCTCTG 2100
QY 2101 AAGAAAGTCAATCCGTTGAGGCTATTCAATATTTCAAGAGTCCATGTGAAGATTC 2160
Db 2101 AAGAAAGTCAATCCGTTGAGGCTATTCAATATTTCAAGAGTCCATGTGAAGATTC 2160
QY 2161 CG 2162
Db 2161 CG 2162

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RESULT 2

AAF88779

ID AAF88779 standard; DNA; 1632 BP.

XX AAF88779;

AC AAF88779;

XX AAF88779;

DT 11-DEC-2002 (first entry)

XX AAF88779;

DE P. amygdalus/A. niger HNL5/box fusion construct PamHNL5xGOX DNA.

XX Almond; hydroxynitrile lyase; HNL5; (R)-cyanohydrin synthesis; vitamin;

KW (S)-cyanohydrin synthesis; pyrethroid; gene; fusion construct;

KW glucose oxidase, ds.

XX Chimeric - Prunus amygdalus.

OS Chimeric - Aspergillus niger.

OS Synthetic.

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XX Key Location/Qualifiers
FH CDS 10..1614
FT /*tag= a
FT /product= "HNL5/glucose oxidase fusion construct"
XX
PN EF1223220-A1.
XX
XX 17-JUL-2002.
XX
XX 18-DEC-2001; 2001EP-0130058.
XX
XX 16-JAN-2001; 2001AT-0000060.
XX
XX 03-APR-2001; 2001AT-0000523.
XX
XX (STAM ) DSM FINE CHEM AUSTRIA NFG GMBH & CO KG.
XX
XX Schwab H, Glieder A, Kratky C, Dreveny I, Poehlauer P, Skranc W;
XX Mayrhofer H, Wirth I, Neuhof R, Bona R;
XX
XX MPI; 2002-645697/70.
XX
XX P-PSDB; AAB71495.
XX
XX New gene for hydroxynitrile lyase from Prunus species, useful for
XX stereospecific synthesis of cyanohydrin -
XX
XX Example 10; Fig 3; 49pp; German.
XX
XX This invention describes a novel gene that encodes a hydroxynitrile lyase
XX (HNL) isolated using one PCR primer based on the 5'-region of the mdl
XX gene of Prunus serotina or P. amygdalus and a second PCR primer, based on
XX the 3'-region of an HNL isoenzyme from the same species. The signal
XX region of the HNL protein can be used for secretory expression of
XX heterologous proteins, e.g. fusion proteins, with NHL activity in host
XX cells. The products of the invention are useful for synthesis of (R)- or
XX (S)-cyanohydrins, e.g. for synthesis of pharmaceuticals, vitamins and
XX pyrethroids. Recombinant expression of HNL produces technically useful
XX amounts of HNL, and these allow stereoselective synthesis of both (R)-
XX or (S)-cyanohydrins. This sequence encodes a fusion construct containing
XX the Prunus amygdalus HNL5 protein and the Aspergillus niger glucose
XX oxidase (Gox) protein described in the method of the invention.
XX
XX Sequence 1632 BP; 451 A; 357 C; 361 G; 463 T; 0 other;
XX
XX Query Match 58.8%; Score 1272; DB 24; Length 1632;
XX Best Local Similarity 88.0%; Pred. No. 0;
XX Matches 1485; Conservative 0; Mismatches 0; Indels 203; Gaps 1;
XX
XX QY 281 TACACGCCACCTGATACAGCTCCGAGGATCATATGACTACATTTGTAATCGGTGAGGA 340
XX Db 94 TACACGCCACCTGATACAGCTCCGAGGATCATATGACTACATTTGTAATCGGTGAGGA 153
XX
XX QY 341 ACATCAGGGTGTCCATTTGGCAGCACTTTATCAGAAAATACAGGTGCTTCTTAGAA 400
XX Db 154 ACATCAGGGTGTCCATTTGGCAGCACTTTATCAGAAAATACAGGTGCTTCTTAGAA 213
XX
XX QY 401 AGAGGCACTATTGCTACAGATACCCGAACACGTTGACTGCAGATGGGTTTGCATATAAT 460
XX Db 214 AGAGGCACTATTGCTACAGATACCCGAACACGTTGACTGCAGATGGGTTTGCATATAAT 273
XX
XX QY 461 CTGCAGCACACAGATGATGGAAGACCGCACTTGAAGGTTCTGTCGAGATGGCAATT 520
XX Db 274 CTGCAGCACACAGATGATGGAAGACCGCACTTGAAGGTTCTGTCGAGATGGCAATT 333
XX
XX QY 521 GATAATGTGCGAGCCAGGATCTCGTGGCAGCAGCAATAATCAATGACGGGTCTTACGCC 580
XX Db 334 GATAATGTGCGAGCCAGGATCTCGTGGCAGCAGCAATAATCAATGACGGGTCTTACGCC 393
XX
XX QY 581 AGAGCTAACTTTCAATTTCTATAGTCAAAACAGGAATTTGAATGGGACCTGGATTTGGTCAAT 640
XX Db 394 AGAGCTAACTTTCAATTTCTATAGTCAAAACAGGAATTTGAATGGGACCTGGATTTGGTCAAT 453
XX
XX QY 641 AAGACATATGAGTGGGTTGAAGACGCCATTTGTGTTCAAGCCAAATAATCAATCTTGGCAA 700

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Db 454 AAGACATATGATGGTGTGAGAGCGCCATTGTGTCAAGCCAAATAATCAATCTTGGCAA 513
Qy 701 TCTGTTATAGAGAGGATCTTGGAGCGGATATCTTCAGACAAATGGAATAGTTTGG 760
Db 514 TCTGTTATAGAGAGGATCTTGGAGCGGATATCTTCAGACAAATGGAATAGTTTGG 573
Qy 761 GATCAGAGAGAGAGATCTAGACTCAGCGGCTCAACTTTTGACAAATAGGAACGCGACAT 820
Db 574 GATCAGAGAGAGAGATCTAGACTCAGCGGCTCAACTTTTGACAAATAGGAACGCGACAT 633
Qy 821 CGCGCTGATGAACTGCTTAATAAGAGAGACCTTAATACCTTGTAGTTGAGTTTCAGGCC 880
Db 634 CGCGCTGATGAACTGCTTAATAAGAGAGACCTTAATACCTTGTAGTTGAGTTTCAGGCC 693
Qy 881 TCAGTAGAGAGATCTCTCTCTTCCCAATACATCAAGATATGTTGCATCAGTGATATTTA 940
Db 694 TCAGTAGAGAGATCTCTCTCTTCCCAATACATCA-----730
Qy 941 ATGGTAGCTCTAGTTTGTGATGCTGCACGCAAAATATTTATCATTTTAAATA 1000
Db 731 -----730
Qy 1001 CTAACAGATAGTGTGAAGTCTCATATTTCCCTTCCATATTTCCCAAATTTCCATAACA 1060
Db 731 -----730
Qy 1061 AACTTCCCAATCTCCTTGGTTAGTTTGAATAATATTAAGCTATTCTTAATGCAG 1120
Db 731 -----730
Qy 1121 ATTTGTGAGCTATTGAGTGCATATATACGATTTCTGATGGAACCTCTCATCAGGCATTG 1180
Db 731 ATTTGTGAGCTATTGAGTGCATATATACGATTTCTGATGGAACCTCTCATCAGGCATTG 790
Qy 1181 TACCGGTTACCGAGAGATTTATCTGTAGTGCAGGACCAATCGGAACCCCTCAGCTTCTAC 1240
Db 791 TACCGGTTACCGAGAGATTTATCTGTAGTGCAGGACCAATCGGAACCCCTCAGCTTCTAC 850
Qy 1241 TACTTAGTGGGTTGACAGAGCTTACCTATCTTCTCAACATCACAGTTGTTTCAGC 1300
Db 851 TACTTAGTGGGTTGACAGAGCTTACCTATCTTCTCAACATCACAGTTGTTTCAGC 910
Qy 1301 CGAATCCTTAGTTGGGCGATTTCTGTATGACATCTCGTATTTTCATTAATTTTGC 1360
Db 911 CGAATCCTTAGTTGGGCGATTTCTGTATGACATCTCGTATTTTCATTAATTTTGC 970
Qy 1361 CCCCAATCCAAATGAAGCCTCTCTGTAACTGTTTAGGCATTAGAGTGATTTATTATC 1420
Db 971 CCCCAATCCAAATGAAGCCTCTCTGTAACTGTTTAGGCATTAGAGTGATTTATTATC 1030
Qy 1421 AAGTTTCTGTGAGCTTGCATTTTCCATCCACCCCTTAGTCTTTTTCCTACAAACAT 1480
Db 1031 AAGTTTCTGTGAGCTTGCATTTTCCATCCACCCCTTAGTCTTTTTCCTACAAACAT 1090
Qy 1481 CTTACCCCTCCCAATTCGACTTTTCTCATATGTTTACCAAGTTCCAGGACCAATTGT 1540
Db 1091 CTTACCCCTCCCAATTCGACTTTTCTCATATGTTTACCAAGTTCCAGGACCAATTGT 1150
Qy 1541 CTCATGTTCTGTCAAGCTAAATTCATCTGACGTGAGAAATCGCTCCAAATATTAAAT 1600
Db 1151 CTCATGTTCTGTCAAGCTAAATTCATCTGACGTGAGAAATCGCTCCAAATATTAAAT 1210
Qy 1601 TCAATTACTATTCAAAATCCACAGACTTGTCTAATTTGTGTAGCGGATGAAGAGCTTG 1660
Db 1211 TCAATTACTATTCAAAATCCACAGACTTGTCTAATTTGTGTAGCGGATGAAGAGCTTG 1270
Qy 1661 GTGACTTTATTAAGCAAGAGCATTAGAACATATAAAGTTCGAGATGCTCGGAAATTG 1720
Db 1271 GTGACTTTATTAAGCAAGAGCATTAGAACATATAAAGTTCGAGATGCTCGGAAATTG 1330
Qy 1721 ACGGTTTCAATTTTGGAGTACTCTTTGCCAGAGAACCAACAGATGATGCATCTCTCG 1780

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Db 1331 ACGTTTCAATTATTTGGAGTACCTTTGCCAGAGAACAAACAGATGATGATCCTTCG 1390
Qy 1781 AAACATTTTGTCTAGATAATGTAGTCTTCACTACTGSCATTACCACGTCGAGCCTTGTG 1840
Db 1391 AAACATTTTGTCTAGATAATGTAGTCTTCACTACTGSCATTACCACGTCGAGCCTTGTG 1450
Qy 1841 GGAAGTGTCTTATGATGACAGTTTCCGTTTATGGGATCAAAAGCATTACGCGTTGTGATG 1900
Db 1451 GGAAGTGTCTTATGATGACAGTTTCCGTTTATGGGATCAAAAGCATTACGCGTTGTGATG 1510
Qy 1901 CCTCCACTTTCCCTTACGACCAACACACGCTTCCTCAGGCTTCTATCTGATGTTAGAA 1960
Db 1511 CCTCCACTTTCCCTTACGACCAACACACGCTTCCTCAGGCTTCTATCTGATGTTAGAA 1570
Qy 1961 GGTATGTG 1968
Db 1571 GGTATGTG 1578

RESULT 3
AAF88780
ID AAF88780 standard; DNA; 2087 BP.
XX
AC AAF88780;
XX
DT 11-DEC-2002 (first entry)
XX
DE Almond HNL1 DNA fragment.
XX
KW Almond; hydroxynitrile lyase; HNL; (R)-cyanohydrin synthesis; vitamin;
KW (S)-cyanohydrin synthesis; pyrethroid; gene; ds.
OS
XX
FH Key
CDS Location/Qualifiers
FT 1..2087
FT /*tag= a
FT /product= "HNL1"
FT /note= "partial CDS with no stop codon. CDS is
FT interrupted by introns"
FT
FT exon 1..103
FT /*tag= b
FT /number= 1
FT 104..249
FT /*tag= c
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FT /*tag= d
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FT 907..1047
FT /*tag= e
FT /number= 2
FT 1048..1888
FT /*tag= f
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FT 1889..1993
FT /*tag= g
FT /number= 3
FT 1994..2087
FT /*tag= h
FT /number= 4
FT /note= "partial, no stop codon given"
XX
PF EP12323220-A1.
XX
PD 17-JUL-2002.
XX
PF 18-DEC-2001; 2001EP-0130058.
XX
PR 16-JAN-2001; 2001AT-0000060.
XX
PR 03-APR-2001; 2001AT-0000523.
XX
PR (STAM ) DSM FINE CHEM AUSTRIA NFG GMBH & CO KG.

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PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145513.
PR 27-JUL-1999; 99US-0145518.
PR 27-JUL-1999; 99US-0145519.
PR 28-JUL-1999; 99US-0145551.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
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PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149829.
PR 23-AUG-1999; 99US-0149802.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 16-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.

PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 26-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 6.4%; Score 138; DB 21; Length 2017;
Best Local Similarity 54.1%; Pred. No. 3.5e-27;
Matches 329; Conservative 0; Mismatches 270; Indels 9; Gaps 2;

QY 311 TCATATGACTACATTTGTAATCGGTGGAGGAACATCAGGTCATTCATTTGGCAGCACTTTA 370
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Db 184 TCCTACGACTACATAGTCATCGGAGGTGGAACCGCAGGGTGTCTCTCGCCGCAACGTTG 243
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 371 TCAGAAAATACAAAGTCTCTTCTAGAAAAGAGCACTATTGCTACAGATATCCCGAAC 430
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 244 TCGCAGATTTTCAGCGTTCTTTGTTTAGAGAGAGGTGGCGTTCCGTTTACAAACGCAAC 303
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 431 AGTTGACTGCAGATGGGTTTGCATATATCTGCAGCAACAAAGATGATGGAAGACGCCA 490
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 304 --GTTTCTCTCCTCAGGAATTTTTCACATCGGACTTGTGACATTTCACTTTCAGTTCT 360
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 491 GTTGAAGGTTCTGTCCTCGAAGATGGCAATTCATATGTCGAGCAGGATCCTCGTGSC 550
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 361 TCTCAAGCGTTGTTTCCACTGACGCGCTTTTACACGCCCTGCTAGAGTTCTCGTGSC 420
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 551 ACGACCAATAATCAATGACGAGGCTTACGCCAGAGCTAACATTTCACTTATAGTCAACA 610
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Db 421 GGTTCCTGTATTAACGCCGGTTTCTCCAGAGCCGATGCTGCTTCTGAAGCGAGCA 480
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QY 611 GGAATTAAGGACCTGGATTTGTCATTAAGACATATAGTGGTTTGAAGACCCATT 670
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Db 481 GG-----ATGGGATCCGAAGCTGGTGAAGGAGTCTATCCATGGGTGGAGAGAGATT 534
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 671 GTGGTCAAGCAATAATCAATCTTGGCAATCTGTTATAGAGAGGAGATTCTTGAGGCG 730
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 535 GTTCATCAGCCCAAGTTAACTTATGGCAGAAAGTCTTCAGAGACAGTCTTTAGAGTT 594
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 731 GGTATTTCTCCAGACAATGGAATTTAGTTTGGATCAAGAGCAGGAACTAGACTCACCGC 790
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Db 595 GGAGTCAGACCTTTCAATGGTTTCACTTACGATCAGCTTCGGGAACCAAAATCGCGGT 654
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QY 791 TCACTTTTGCATAATTAAGAACCGGACATCGCGCTGATGACTCTTAATAAAGAGAC 850
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Db 655 ACAATTTTCAGAGATTCGCGCGTCTCACACCGCGGCGAGCTTCTCGCTTACGCTAAT 714
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Db 715 CCTCAGAGCTTAGAGTCTTGATCTACGCCACCGTGCAGAAAATGCTTTTGACACTTCT 774
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QY 911 ACATCAAG 918
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RESULT 5
AAC50934
ID AAC50934 standard; DNA; 2104 BP.
XX
AC AAC50934;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 66674.
XX
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KW Hybridization assay; genetic mapping; gene expression control;
 KW protein identification; signal transduction pathway;
 KW metabolic pathway; promoter; termination sequence; ss.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121625.

XX 05-MAR-1999; 99US-0123180.

XX 09-MAR-1999; 99US-0123548.

XX 23-MAR-1999; 99US-0125788.

XX 25-MAR-1999; 99US-0126264.

XX 29-MAR-1999; 99US-0126785.

XX 01-APR-1999; 99US-0127462.

XX 06-APR-1999; 99US-0128234.

XX 08-APR-1999; 99US-0128714.

XX 16-APR-1999; 99US-0129845.

XX 19-APR-1999; 99US-0130077.

XX 21-APR-1999; 99US-0130449.

XX 23-APR-1999; 99US-0130510.

XX 23-APR-1999; 99US-0130891.

XX 28-APR-1999; 99US-0131149.

XX 30-APR-1999; 99US-0132048.

XX 30-APR-1999; 99US-0132407.

XX 04-MAY-1999; 99US-0132484.

XX 05-MAY-1999; 99US-0132485.

XX 06-MAY-1999; 99US-0132486.

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XX 07-MAY-1999; 99US-0132863.

XX 11-MAY-1999; 99US-0134256.

XX 14-MAY-1999; 99US-0134218.

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XX 27-MAY-1999; 99US-0136392.

PR 23-JUN-1999; 99US-0140354.
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 PR 28-JUN-1999; 99US-0140823.
 PR 29-JUN-1999; 99US-0140991.
 PR 30-JUN-1999; 99US-0141287.
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PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match
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Matches 329; Conservative 0; Mismatches 270; Indels 9; Gaps 2;

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QY 371 TCAGAAAATACAGGTGCTTCTTCTAGAGAGGACATATTCCTACAGATATACCGAAC 430
DB 346 TCGCAGATTTACGGTCTCTTTTGTAGAGAGGTGGCGTTCGTTTACAAACGCAAC 405
QY 431 ACCTTGACTCAGATGGGTTTGCATATATCTGCAGCAACAGATGATGGAAGACGCCA 490
DB 406 --GTTTCTTCTCAGAAATTTTCATCTCGACTGCTGCATTTTCAGCTTCTTCGCG 462
QY 491 GTTGAAAGTTCGTGTCGAGATGCGATTAATGATGAGCGAGGATTCCTCGGTGGC 550
DB 463 TCTCAGCGTTGTGTTTCCCTAGCGGGTTTACACCGCGCTGAGAGTCTCGGTGGC 522
QY 551 ACGACCAATATCAATGACGCGTCTACCGAGCTTAACATTTTCATCTATAGTCAACA 610
DB 523 GGTTCCTGTTATACGCCGGTTTATCTCAGAGCGGATGCTCGGTTCGTTGAGACGCA 582
QY 611 GGAATTGAATGGCACTGGATTTGGTCAATAGACATATGATGGGTGGTTGAGACGCCATT 670

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Db 583 GG-----ATGGATCCGGAAGCTGGTGAAGAGTCTGTATCCATGGGTGGAGAGAGATT 636
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Db 637 GTTCATCAGCCAAAGTTAAGCTTATGGCAGAAAGCTCTCAGAGACAGTCTTTTAGRGTT 696
QY 731 GGTATTCITTCAGACAAATGGATTTAGTTTGGATCAAGAGCAGGAACTAGACTCACCGGC 790
Db 697 GGAGTCAGACCTTTCAATGGTTTCACTTACGATCAGTTTCCGGAACCAAAATCGCGGT 756
QY 791 TCAACTTTTGACAATAATGGRACGCGACATGCGGCTGTGACTGCTTAATTAAGAGAC 850
Db 757 ACAATTTTCGACAGATTCGCGCTGTCTACACCGCGGAGCTTCTCGCTTACGCTAAT 816
QY 851 CCTAATACTTGTAGTTGCACTTCAGGCTCAGTAGAGAGAGATCTCTTCTTCCCAAT 910
Db 817 CCTCAGAGCTTAGAGTCTTGATCTACGCCACCGTGCAAAAATCGTCTTTGACACTTCT 876
QY 911 ACATCAAG 918
Db 877 GGAACAAG 884

RESULT 6
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DT 21-JAN-2003 (first entry)
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DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2174.
XX
KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO200216655-A2.
XX
PD 28-FEB-2002.
XX
PF 24-AUG-2001; 2001WO-US26685.
PR 24-AUG-2000; 2000US-227866P.
PR 26-JAN-2001; 2001US-264647P.
PR 22-JUN-2001; 2001US-300111P.
XX
(SCRI ) SCRIPPS RES INST.
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
Harper JF, Kreps J, Wang X, Zhu T;
XX
WPI; 2002-304127/34.
XX
Identifying a stress condition to which a plant cell has been exposed
and producing plants with increased tolerance to these abiotic stresses
XX
Claim 144; SEQ ID NO 2174; 577pp + Sequence Listing; English.
XX
The invention relates to identifying a stress condition to which a plant
cell has been exposed, comprising:
CC (a) contacting nucleic acid representative of expressed polynucleotides
in the plant cell with an array or probes representative of the plant
cell genome; and
CC (b) detecting a profile of expressed polynucleotides in the plant cell
characteristic of a stress response. The method is useful in the
CC production of transgenic plants, cells and seeds and in producing plants
with increased tolerance to abiotic stress. The present sequence is that
CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
in methods of the invention.
CC Note: The sequence data for this patent is not represented in the printed
specification but is based on sequence information supplied to Derwent by

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CC	the European Patent Office.		
XX	Sequence 1854 BP; 542 A; 371 C; 438 G; 503 T; 0 other;		
SQ	Query Match 6.0%; Score 129.4; DB 24; Length 1854;		
	Best Local Similarity 52.2%; Pred. No. 7.6e-25;		
	Matches 314; Conservative 0; Mismatches 281; Indels 6; Gaps 1;		
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DB	688 TCGAGCGCTATCAATGGCGGATTTTACAGCCGAGCTAGCGATGAGTTTGTGAAGAAAGCT 747	PR	16-APR-1999; 99US-0129845.
QY	611 GGAATTCATGCGACCTGGATTTGGTCAATAAGACATATGAGTGGTGTGAAGACGCCATT 670	PR	19-APR-1999; 99US-0130077.
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XX		PR	21-MAY-1999; 99US-0135353.
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KW	metabolic pathway; promoter; termination sequence; ss.	PR	01-JUN-1999; 99US-0137222.
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PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
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PR 29-OCT-1999; 99US-0162142.

Query Match 5.7%; Score 123.4; DB 21; Length 1837;
Best Local Similarity 53.2%; Pred. No. 3.3e-23;
Matches 312; Conservative 0; Mismatches 266; Indels 9; Gaps 2;

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QY 374 GAAATAACAAGTGTCTTCTTAGAAAGAGGCACCTATTGTGACAGAAATACCCGAACAG 433
DB 249 CAAACGCCAGCGTTTGTCTGCTCGAACCGGTGACTCACCCTACATAACCCCAACATC 308
QY 434 TTGACTGCGAGTGGTGTTCGATATATCTGCGAGCAACAGATGATGGAAGAGCCGCTT 493
DB 309 ACGAGGCTCTCGGCTTTTCGGGCGGCTCTCTGACCTGTCTGAGTCCT---CACCATCT 365
QY 494 GAAAGGTTCGTGCCGAAGATGSCATTGATGTCGAGCCAGGATCTCTCGTGGCAGC 553
DB 366 CAGCGTTTGTATCAGAAGATGTGTCTATATGACGTGCTCGGGTCTCGGTGGCGGA 425
QY 554 ACCATATCAATGCGAGCGTCTACGCGAGAGCTAACATTTCATTATAGTCAAAACAGGA 613
DB 426 AGCGCTCTCAACCGCGCTTCTATACACGTGCGGCGCTAAATACGTTAGGAACATGGG- 484
QY 614 ATTGAATGGACCTGATTTGGTCTAATAGACATATGATGATGGTGTGAAGACGCCATTG 673
DB 485 -----TTGGGACGGAGCGCTAGCGAACGAGTGTGACCTGAGTGTGAAGTGGGG 539
QY 674 GTCAGCCAAATAATCAATCTTGGCAATCTGTTATAGGAGAGGATCTTTGAGGCGGT 733
DB 540 TTTCAGCCTCCGATGGGGCGGTGGGCAACCGCGGTGAGAGAGCGGCTTATTGAGGGTGG 599
QY 734 ATTCTTCCAGACAATGGATTTAGTTTGGATTCAGAGAGAGGAACTAGACTCCCGGCTCA 793
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PR	13-AUG-1999;	99US-0148684;	QY	431	ACGTTGACTGCAGATGGGTTTCCATATATCTGCAGCAACAGATGATGAGAGAGCCCA	490
PR	16-AUG-1999;	99US-0149368;	DB	398	GTTT---CTTCTCAGGAATTTTACATCGGACCTTCTGACATTTACGCTTCTCCGCG	454
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PR	20-AUG-1999;	99US-0149722;	DB	455	TCTCAGCGTTTGTTCCTCACTGACGGGTTTACACGCTCGTCTAGAGTTCTCGTGGC	514
PR	20-AUG-1999;	99US-0149723;	QY	551	ACGACCAATTAATCAATGACGGGCTTACGCCAGAGCTAACATTTTCAATTTCTATAGTCAACA	610
PR	20-AUG-1999;	99US-0149929;	DB	515	GGTTCTGTATTAAAGCCCGTTTCTACTCCAGAGCGATGCTGCGTTCTGTAAGCGAGCA	574
PR	23-AUG-1999;	99US-0149902;	QY	611	GGAAATTGAATGGGACCTGGATTTGGTCAATAGACATATGACTGGGTTTGAAGACGCCATT	670
PR	23-AUG-1999;	99US-0149930;	DB	575	GG-----ATGGATCCGGAAGCTGGTGAAGGAATCGTATCCATGGGTGGAGAGAGATT	628
PR	25-AUG-1999;	99US-0150566;	QY	671	GTGGTCAAGCCAAATAATCAATCTTGGCAATCTGTATAGGAGAGAGGATTTCTTGGAGCG	730
PR	26-AUG-1999;	99US-0150884;	DB	629	GTTTCATCAGCCAAAGTTAAGTTATGGCAGAAAGCTCTCAGAGACAGTCTTTTAGAGGTT	688
PR	27-AUG-1999;	99US-0151065;	QY	731	GGTATTTCTCCAGACAAATGGATTTAGTTGGATTCAGAAAGGAGGAACTACAGCTCACCGG	790
PR	27-AUG-1999;	99US-0151086;	DB	689	GGAGTCAGACCTTTTCAATGGTTTTCACCTACGATCAGCTCCCGGAACCAAAATCGCGGG	748
PR	30-AUG-1999;	99US-0151303;	QY	791	TCAACTTTTGACATAATGGAAGCGGACATGCGGCTGTGATGAATGCTTAAATAAGGAGAC	850
PR	31-AUG-1999;	99US-0151438;	DB	749	ACAAATTTTCGATAGATTCGCGCGTGTGACAGCGCGGCGAGCTTCTCGCTTACGCTAAT	808
PR	01-SEP-1999;	99US-0151930;	QY	851	CCTAATAACTTCTAGTTGCACTTACGCTTACGAGCTTACGAGCTCAGTAGAGAAATCCTCTT	900
PR	07-SEP-1999;	99US-0152363;	DB	809	CCTCAGAAGCTTAGAGTCTTGATCTACGCCACTGTGCAAAAATCGTCTT	858
PR	10-SEP-1999;	99US-0153070;	PR	AAAF88763	standard; DNA; 68 BP.	
PR	13-SEP-1999;	99US-0153758;	AC	AAAF88763;		
PR	15-SEP-1999;	99US-0154018;	XX	11-DEC-2002	(first entry)	
PR	16-SEP-1999;	99US-0154039;	DT	Almond HNL5	PCR primer PamHNL5a2 SEQ ID 4.	
PR	20-SEP-1999;	99US-0154779;	DE	Almond;	hydroxynitrile lyase; HNL; (R)-cyanohydrin synthesis; vitamin;	
PR	22-SEP-1999;	99US-0155139;	KW	(S)-cyanohydrin	synthesis; pyrethroid; PCR; primer; ss.	
PR	23-SEP-1999;	99US-0155486;	KW	Prunus amygdalus.		
PR	28-SEP-1999;	99US-0156458;	OS	EP1223220-A1.		
PR	29-SEP-1999;	99US-0156596;	PN	17-JUL-2002.		
PR	04-OCT-1999;	99US-0157117;	PD	18-DEC-2001;	2001EP-0130058.	
PR	05-OCT-1999;	99US-0157753;	XX	16-JAN-2001;	2001AT-0000060.	
PR	06-OCT-1999;	99US-0157865;	XX	03-APR-2001;	2001AT-0000523.	
PR	07-OCT-1999;	99US-0158029;	XX	(STAM)	DSM FINE CHEM AUSTRIA NFG GMBH & CO KG.	
PR	08-OCT-1999;	99US-0158232;	PI	Schwab H, Glieder A, Kratky C, Dreveny I, Foehlauer P, Skranc W;		
PR	12-OCT-1999;	99US-0158369;	PI	Mayrhofer H, Wirth I, Neuhofer R, Bona R;		
PR	13-OCT-1999;	99US-0159293;	DR	WPI; 2002-645697/70.		
PR	13-OCT-1999;	99US-0159294;	XX	New gene for hydroxynitrile lyase from Prunus species, useful for		
PR	13-OCT-1999;	99US-0159295;	PT	stereospecific synthesis of cyanohydrin -		
PR	14-OCT-1999;	99US-0159329;	XX	Example 4; Page 7; 49pp; German.		
PR	14-OCT-1999;	99US-0159330;	PR			
PR	14-OCT-1999;	99US-0159331;	QY			
PR	14-OCT-1999;	99US-0159637;	DB			
PR	14-OCT-1999;	99US-0159638;				
PR	18-OCT-1999;	99US-0159584;				
PR	21-OCT-1999;	99US-0160741;				
PR	21-OCT-1999;	99US-0160767;				
PR	21-OCT-1999;	99US-0160768;				
PR	21-OCT-1999;	99US-0160770;				
PR	21-OCT-1999;	99US-0160814;				
PR	21-OCT-1999;	99US-0160815;				
PR	22-OCT-1999;	99US-0160980;				
PR	22-OCT-1999;	99US-0160981;				
PR	22-OCT-1999;	99US-0160989;				
PR	25-OCT-1999;	99US-0161404;				
PR	25-OCT-1999;	99US-0161405;				
PR	25-OCT-1999;	99US-0161406;				
PR	26-OCT-1999;	99US-0161359;				
PR	26-OCT-1999;	99US-0161360;				
PR	26-OCT-1999;	99US-0161361;				
PR	28-OCT-1999;	99US-0161920;				
PR	28-OCT-1999;	99US-0161922;				
PR	28-OCT-1999;	99US-0161993;				
PR	29-OCT-1999;	99US-0162142;				

Query Match 5.7%; Score 122.4; DB 21; Length 2098;
 Best Local Similarity 54.1%; Pred No. 5.7e-23;
 Matches 319; Conservative 0; Mismatches 261; Indels 10; Gaps 3;
 QY 311 TCATATGACTACATTTGATCGGTGAGGAGCAATCAGGGTCTCCATTTGGCAGCAACTTTA 370
 DB 279 TCCTACGACTACATAGTATCATCGGAGGTGGRACCGCA-GGTGCTCTCTCGCGCAACGTTG 337

encoded protein, and mapping functional regions of protein -
 Claim 1; SEQ ID NO 404; 49pp + Sequence Listing; English.

The invention relates to an Arabidopsis thaliana nucleic acid (I) comprising a sequence capable of hybridising under stringent conditions to a sequence selected from any one of 999 sequences (ABN98233-ABN99231), given in the specification or its fragment. A polypeptide (II) encoded by (I), a transgenic plant (III) comprising an exogenous nucleic acid or a genetically modified cell (IV) comprising an exogenous nucleic acid, is useful for screening a candidate agent for its biological effect. (I) is useful in identifying homologous or related genes, in producing compositions that modulate the expression or function of its encoded protein, mapping functional regions of the protein and in studying associated physiological pathways. (I) is also useful for the genetic manipulation of cells, particularly plant cells. (I) is also useful in screening assays of various plant strains to determine the strains that are best capable of withstanding a particular disease or environmental stress. (II) and (III) are useful for screening of biologically active agents, e.g. fungicides, insecticides, etc., for elucidating biochemical pathways. The screened agents are useful in improved methods of treating crops to prevent or treat disease. (II) are also useful in screening programs to identify agents that mimic or enhance the action of tolerance factors. Such agents are useful in improved methods of treating crops to enhance their tolerance to environmental stress. (I) is also useful for enhancing or inhibiting production of a biosynthetic product in a plant. (III) is useful for identifying other mediators that may induce expression of proteins of interest, for establishing the extent to which any specific insect and/or pathogen is responsible for damage to a particular plant, for identifying other mediators that enhance or induce tolerance to environmental stress, for identifying factors involved in biosynthetic pathways of nutritional, commercial, or medicinal value and for identifying productions of nutritional, commercial or medicinal value. (IV) is useful in the study of genetic function and regulation, for alteration of the cellular metabolism and for screening compounds that may affect the biological function of the gene or gene products. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?docID=999909770445.

Sequence 925 BP; 268 A; 190 C; 182 G; 285 T; 0 other;
 Query Match 2.8%; Score 60.6; DB 24; Length 925;
 Best Local Similarity 53.6%; Pred. No. 4e-06;
 Matches 126; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

1749 GCCAGAGCAACCAACAGATGATGCTCTTCGAAACATTTTGTCTAGATATAGCTTC 1808
 571 GCCAAGCAACTGAACGTACCAATCAATGGCTCAGTTCTGCAAGACACTGTGTAC 512
 1809 ATACTGGCATPACACGGTGAAGCCTTTGTTGGAAAGTCTTGATGACAGTTCCGTGT 1868
 511 AATCTGGCACTACCATGCTGTGATGCTTTGTGGGTAAAGTTGTGAGCCCTAACCGCAAGT 452
 1869 TATGGGATCAACGATTAACGCTGTGATGCTCTCCACTTCCCTTACGACCAACAG 1928
 451 TCITGGTGTGACAGGCTCAGAGTTATGTAGTGTTCACCGTTTGACGAGTCTCCAGAAC 392
 1929 CCATCCTCAGGGCTTCTATCTGATGTTAGGAAGTATGTGATGACACTTCCCAAC 1983
 391 CAACCGCAAGCTACTATGATGATGATGCGGAAGTAAATCAATCATTACCAAC 337

RESULT 12
 ABL73822
 ID ABL73822 standard; cDNA; 300 BP.

AC ABL73822;

14-MAY-2002 (first entry)

Corn tassal-derived polynucleotide (cdps) SEQ ID NO:3196.

Corn; corn tassal-derived polynucleotide; cdps; hybrid breeding; CDPS; inheritance; characteristic; growth; development; disease resistance; environmental adaptability; quality; yield; molecular marker; multigene trait; plant breeding; corn tassal; gene; ss.

Zea mays.
 US2001051335-A1.
 13-DEC-2001.
 16-APR-1999; 99US-0294093.
 21-APR-1998; 98US-082567P.

(LALG/) LALGUDI R V.
 (ITOL/) ITO L Y.
 (SHER/) SHERMAN B K.

Lalgudi RV, Ito LY, Sherman BK;
 WPI; 2002-163647/21.

Novel purified corn tassal-derived polynucleotide useful for determining altered gene expression, to recover regulatory elements and to follow inheritance of desirable characteristics through hybrid breeding programs -

Claim 1; SEQ ID 3196; 201pp; English.

The present sequence describes a purified corn tassal-derived polynucleotide sequence (cdps) comprising a nucleic acid sequence selected from those given in ABL70627 to ABL76833. The cdps sequences encode corn tassal-derived polypeptides (CDPS). The cdps sequences (I) can be used for determining altered gene expression, to recover regulatory elements and to follow inheritance of desirable characteristics through hybrid breeding programs. (I) are also useful in the evaluation, and alteration of desired characteristics associated with growth and development, disease resistance, environmental adaptability, quality and yield, and as molecular markers for studying inheritance of multigene traits in a plant breeding program. (I) can be used to produce a tassal-specific profile of gene transcription, a transcript image, to clone regulatory elements for use in transfection vectors, to express a polypeptide, to identify, isolate or extend identical or related corn tassal nucleic acid sequences from DNA libraries, in nucleic acid hybridisation or amplification technologies, as query sequences to determine homology of known sequences, as probe for use in Southern or Northern hybridisation, and to identify the presence of and/or to determine the degree of similarity between two (or more) nucleic acid sequences.

Sequence 300 BP; 81 A; 59 C; 87 G; 72 T; 1 other;

Query Match 2.7%; Score 59.4; DB 24; Length 300;
 Best Local Similarity 61.1%; Pred. No. 5.1e-06;
 Matches 96; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

1812 CTGGCATACCGGTGGAGCCTTTGGGAAAGTCTTGATGACAGTTCCGTGTAT 1871
 119 CTGGCATATATCATGTTGGTGGTGCCTATGTAGGGAAGTGTGACCGGTTGT 178
 1872 GGCGATCAAGCATTAACGCTTTGATGCTCTCCACTTCCCTTACGACCAACAGCA 1931
 179 TGAAGTTTCAGGCTCTCCGGTGTGTGACGGCTCATATTTCTATATCGCAGGACCA 238
 1932 TCCTCAGGGCTTCTATCTGATGTTAGGAAGTATGTG 1968
 239 CCCTCAAGCTACAGTTATGATGATGCGCAGATATG 275

RESULT 13
 AAH87692
 ID AAH87692 standard; cDNA; 645 BP.

AAH87692;
25-SEP-2001 (first entry)
Peppermint plant oil gland expressed cDNA 48.
Peppermint; plant oil gland cell; terpenoid essential oil; resin;
genetic mapping; antisense suppression; recombinant expression; ss.
Mentha x piperita.
W0200153319-AL.
26-JUL-2001.
19-JAN-2001; 2001WO-US02567.
20-JAN-2000; 2000US-0177264.
(CROT/) CROTEAU R B.
(LANG/) LANGE B M.
(WILD/) WILDUNG M R.
Croteau RB, Lange BM, Wildung MR;
WPI; 2001-488706/53.
New nucleic acid molecules corresponding to mRNA molecules expressed in
peppermint oil glands for enhancing expression of plant oil gland cell
proteins -
Claim 1; Page 95; 251pp; English.
The invention relates to nucleic acid molecules (AAH87645-AAH88116) that
correspond to all or part of a mRNA molecule expressed in plant oil
gland cells, especially peppermint and plant oil glands that produce
terpenoid essential oils and resins. The nucleic acids are useful for
genetically mapping a plant genome for genes expressed in plant oil
gland cells and to suppress (for example by antisense suppression) or
enhance their expression (for example by genetically transforming a
plant cell with a replicable expression vector that expresses one or more
proteins naturally expressed in plant oil gland cells). The nucleic acids
are also useful for recombinant expression of plant oil gland proteins
required for terpenoid essential oil and/or resin production in bacterial
and/or yeast cells.
Query Sequence 645 BP; 194 A; 129 C; 132 G; 189 T; 1 other;
Query Match 2.7%; Score 59.2; DB 22; Length 645;
Best Local Similarity 54.1%; Pred. No. 8.3e-06;
Matches 118; Conservative 1; Mismatches 99; Indels 0; Gaps 0;
QY 1758 CCAACAGATGATGCATCCCTCGAACAATTTTGTCTAGATAATGCTTCACTCTGCA 1817
Db 210 CAATTCAGCAGCTTATAATATGAGAGCATTTTTCATGACACGCTTATGCAATATGCA 269
QY 1818 TTACACGGTGGAGCCCTTGTGGGAAGTCTTGTATGACAGAGTTTCCTGTATGGGGAT 1877
Db 270 TTATCATGGAGTTGCCAAGTGAATCGAGTCTTGATCGCATATTAAGGTGTTCCGAGT 329
QY 1878 CAAAGCATTACCGGTTGTGATGCTTCCACTTCCCTTACGAACCAACAGCCATCTCTCA 1937
Db 330 GGATTCGTTGGCGTTATTGATGGCTCGACGTTTGACTACTCTCCCGGACTATATCTCTCA 389
QY 1938 GGGCTTCTATCTGATGTTAGGAAGGTATGTGATGACA 1975
Db 390 GGCTACAGTTATGATGCTTGGGAGGTATATGGGACAGA 427
RESULT 14
ABL72070
ID ABL72070 standard; cDNA; 276 BP.

Fri Dec 19 06:09:38 2003

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2003, 17:27:04 ; Search time 1794 Seconds

(without alignments)
4015.732 Million cell updates/sec

Title: US-10-046-232-19

Perfect score: 2162

Sequence: 1 ggaattccaatatgagaa.....agtcattgtgaagaattccg 2162

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2211978 seqs, 1666101734 residues

Total number of hits satisfying chosen parameters: 4423956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1202.4	55.6	2087	15	US-10-046-232-23
4	129.4	6.0	1854	10	US-09-938-842A-2174
5	68	3.1	68	15	US-10-046-232-4
6	65.6	3.1	499	11	US-09-770-961-453
7	65	3.0	73	15	US-10-046-232-9
8	60.6	2.8	925	9	US-09-770-445-404
9	59.4	2.7	300	9	US-09-294-093B-3196
10	58.6	2.7	276	9	US-09-294-093B-1444
11	54.6	2.5	441	9	US-09-770-444-909
12	51.2	2.4	267	10	US-09-878-574-207
13	49	2.3	64	15	US-10-046-232-3
14	46.6	2.2	66	15	US-10-046-232-8
15	46.2	2.1	6641	13	US-10-311-455-287

16	46.2	2.1	6641	13	US-10-240-452-35	Sequence 35, Appl
17	45.4	2.1	114	15	US-10-046-232-10	Sequence 10, Appl
18	43.4	2.0	37973	13	US-10-311-455-2169	Sequence 2169, Ap
c 19	42.8	2.0	7607	13	US-10-240-485-168	Sequence 168, App
c 20	41.8	1.9	3673778	13	US-10-312-841-2	Sequence 2, Appli
c 21	41.2	1.9	1595	11	US-09-764-891-326	Sequence 326, App
c 22	41	1.9	6056	13	US-10-311-455-1000	Sequence 1000, Ap
c 23	41	1.9	9268	13	US-10-311-455-1573	Sequence 1573, Ap
24	40.6	1.9	747	13	US-10-140-472-212	Sequence 212, App
25	40.6	1.9	747	13	US-10-141-761-212	Sequence 212, App
26	40.6	1.9	747	13	US-10-142-885-212	Sequence 212, App
27	40.6	1.9	747	13	US-10-158-790-212	Sequence 212, App
28	40.6	1.9	747	13	US-10-137-871-212	Sequence 212, App
29	40.6	1.9	747	13	US-10-140-805-212	Sequence 212, App
30	40.6	1.9	747	13	US-10-140-864-212	Sequence 212, App
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32	40.6	1.9	747	13	US-10-141-756-212	Sequence 212, App
33	40.6	1.9	747	13	US-10-141-759-212	Sequence 212, App
34	40.6	1.9	747	15	US-10-123-155-212	Sequence 212, App
35	40.6	1.9	747	16	US-10-146-731-212	Sequence 995, App
36	40.6	1.9	16236	13	US-10-311-455-995	Sequence 87, Appli
37	40.4	1.9	271990	13	US-10-195-144-87	Sequence 1, Appli
c 38	40.2	1.9	3673778	13	US-10-312-841-1	Sequence 229, App
c 39	40	1.9	2527	9	US-09-822-849A-229	Sequence 28, Appli
c 40	40	1.9	4043	10	US-09-989-920-28	Sequence 3, Appli
c 41	40	1.9	6527	13	US-10-356-631-3	Sequence 1919, Ap
c 42	40	1.9	16811	13	US-10-311-455-1919	Sequence 197239,
43	39.6	1.8	663	13	US-10-027-632-197239	Sequence 197240,
44	39.6	1.8	663	13	US-10-027-632-197240	Sequence 197239,
45	39.6	1.8	663	14	US-10-027-632-197239	

ALIGNMENTS

RESULT 1

US-10-046-232-19

; Sequence 19, Application US/10046232

; Publication No. US20030119099A1

; GENERAL INFORMATION:

; APPLICANT: Helmut SCHWAB

; APPLICANT: Anton GLIEDER

; APPLICANT: Christoph KRATKY

; APPLICANT: Ingrid DREVENY

; APPLICANT: Peter POCHLAUER

; APPLICANT: Wolfgang SKRANC

; APPLICANT: Herbert MAYRHOFER

; APPLICANT: Irma WIRTH

; APPLICANT: Rudolf NEUHOFFER

; APPLICANT: Rodolfo BONA

; TITLE OF INVENTION: New genes containing a DNA sequence coding for a hydroxynitrile

; TITLE OF INVENTION: recombinant proteins derived therefrom and having hydroxynitrile

; FILE REFERENCE: 2001-1882A/LC/01553

; CURRENT APPLICATION NUMBER: US/10/046,232

; CURRENT FILING DATE: 2002-10-31

; PRIOR APPLICATION NUMBER: A60/2001

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: A523/2001

; PRIOR FILING DATE: 2001-04-03

; SOFTWARE: Patent in Ver. 2.1

; SEQ ID NO 19

; LENGTH: 2162

; TYPE: DNA

; ORGANISM: Prunus amygdalus

US-10-046-232-19

Query Match 100.0%; Score 2162; DB 15; Length 2162;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

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Db 1 GGAATTCACAAATATGGAAGAAATCAAAATGTCAATATATTTGTTGTCATCTTCT 60
QY 61 GTTCTTCATCTTCAGTATTCAGAGGTTCACTCGCTTCGCCAATATCTTCGCTCATGGTAA 120
Db 61 GTTCTTCATCTTCAGTATTCAGAGGTTCACTCGCTTCGCCAATATCTTCGCTCATGGTAA 120
QY 121 TTTCCATCTTCAGTATTCATTTAAACAGAAAATGTGTAGATTTTATATTAAGAAAACCTGA 180
Db 121 TTTCCATCTTCAGTATTCATTTAAACAGAAAATGTGTAGATTTTATATTAAGAAAACCTGA 180
QY 181 CACAGTAGTGCAGAAACAGCTAAATTTAGATGCATGTTGAAAATAATCTTCATCTCT 240
Db 181 CACAGTAGTGCAGAAACAGCTAAATTTAGATGCATGTTGAAAATAATCTTCATCTCT 240
QY 241 TCACATATATTTTCAGATTTTACCTACTTGAAGTTTGTACAAACCCACTGATACAAG 300
Db 241 TCACATATATTTTCAGATTTTACCTACTTGAAGTTTGTACAAACCCACTGATACAAG 300
QY 301 CTCGGAAGGATCATATGACATATGTAATCGGTGGAGGAACATCAGGGTGTCCATTGGC 360
Db 301 CTCGGAAGGATCATATGACATATGTAATCGGTGGAGGAACATCAGGGTGTCCATTGGC 360
QY 361 AGCACTTTATCAGAAAATACAGGTGCTTCTCTAGAAAGAGGCACTATTGCTACAGA 420
Db 361 AGCACTTTATCAGAAAATACAGGTGCTTCTCTAGAAAGAGGCACTATTGCTACAGA 420
QY 421 ATACCCGAAACAGCTTGTCTGAGATGGTTGTCATATAATCTGCAGCAACAAGATGATGG 480
Db 421 ATACCCGAAACAGCTTGTCTGAGATGGTTGTCATATAATCTGCAGCAACAAGATGATGG 480
QY 481 AAAGACGCGAGTTGAAGGTTGGTCCGAGATGGCAATGATTAATGTGGAGCGAGAT 540
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QY 541 CCTCGGTGGCAAGCAATATCAATGAGGGTCTAGCCAGAGCTTAACATTTCAATCTTA 600
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Db 601 TAGTCAAAACAGGAATGAATGGGACCTGGATTTGGTCAATAAGACATATCAGTGGGTTGA 660
QY 661 AGAGCCATGTGTCAAGCCAAATAATCAATCTGGCAATCTGTATATAGAGAGAGGAT 720
Db 661 AGAGCCATGTGTCAAGCCAAATAATCAATCTGGCAATCTGTATATAGAGAGAGGAT 720
QY 721 CTTGGAGCGGGTATCTTCAGACAAATGGATTTAGTTTGGATCAGCAAGCAGGACTAG 780
Db 721 CTTGGAGCGGGTATCTTCAGACAAATGGATTTAGTTTGGATCAGCAAGCAGGACTAG 780
QY 781 ACTCACCGGCTCAACTTTTGACAAATATGGAACGCGACATGCGGCTGATGAATCTGTAA 840
Db 781 ACTCACCGGCTCAACTTTTGACAAATATGGAACGCGACATGCGGCTGATGAATCTGTAA 840
QY 841 TAAAGGAGACCTTAATTAATCTGTAGTTGAGTTGAGGCTCAGTAGAAGATTCCTTT 900
Db 841 TAAAGGAGACCTTAATTAATCTGTAGTTGAGTTGAGGCTCAGTAGAAGATTCCTTT 900
QY 901 CTTCTTCAATACATCAAGTATGTTGCATCAGTGATATTTAATGCTAGCTCCTAGTTTGTG 960
Db 901 CTTCTTCAATACATCAAGTATGTTGCATCAGTGATATTTAATGCTAGCTCCTAGTTTGTG 960
QY 961 ATGCTGCACCTCGAAAATTTATTTATCAATTTTAAATAATCAACAGATAGTGTGAAGT 1020
Db 961 ATGCTGCACCTCGAAAATTTATTTATCAATTTTAAATAATCAACAGATAGTGTGAAGT 1020
QY 1021 CTCATATTTCCCTTCATATTTCCCAATTTCCAAATTTCCAAACAAACTTCCCAATTTCTCTTC 1080
Db 1021 CTCATATTTCCCTTCATATTTCCCAATTTCCAAATTTCCAAACAAACTTCCCAATTTCTCTTC 1080
QY 1081 GTTTAGTTTGAACAATTAATAGCTATTTCTCAATGCAATTTGTGAGCTATTTGAGTCT 1140

Db 1081 GTTTAGTTTGAACAATTAATTAAGCTATTTCTCAATGCAATTTGTGAGCTATTTGAGTCT 1140
QY 1141 ATATATATACGATTTCTGATGGAACTCTCATCAGGCAATTTGTACGGGTAAACGGGAAGTT 1200
Db 1141 ATATATATACGATTTCTGATGGAACTCTCATCAGGCAATTTGTACGGGTAAACGGGAAGTT 1200
QY 1201 ATTGTTAGTGCAGGCAATCGGAACGCTCAGCTTTCTACTACTTAGTGGGTGGACCA 1260
Db 1201 ATTGTTAGTGCAGGCAATCGGAACGCTCAGCTTTCTACTACTTAGTGGGTGGACCA 1260
QY 1261 GAGTCTTACCTATCTCTCTCAACATCAGAGTGTTCAGCGGAATCTTATGTGGGAG 1320
Db 1261 GAGTCTTACCTATCTCTCTCAACATCAGAGTGTTCAGCGGAATCTTATGTGGGAG 1320
QY 1321 TTTGTTGATGACAACTCTCGTAAATTTCAATTAATTTTGGCCCAAAATCCCAATGAGCC 1380
Db 1321 TTTGTTGATGACAACTCTCGTAAATTTCAATTAATTTTGGCCCAAAATCCCAATGAGCC 1380
QY 1381 TCTGTTGATGACAACTCTCGTAAATTTCAATTAATTTTGGCCCAAAATCCCAATGAGCC 1440
Db 1381 TCTGTTGATGACAACTCTCGTAAATTTCAATTAATTTTGGCCCAAAATCCCAATGAGCC 1440
QY 1441 CCATTTTCCACTCCACCTTTTAGTCTTTTCTCCTACAACATCTTACCCCTCCCAATTCG 1500
Db 1441 CCATTTTCCACTCCACCTTTTAGTCTTTTCTCCTACAACATCTTACCCCTCCCAATTCG 1500
QY 1501 ACTTTTGTCTCATATTTAGCCAACTTCAGGACCAATTTGTCTCATGTTCTGTACGCTA 1560
Db 1501 ACTTTTGTCTCATATTTAGCCAACTTCAGGACCAATTTGTCTCATGTTCTGTACGCTA 1560
QY 1561 AATTCAATCATCTGAGCGGAGAAATCGCTCCAAATATTAATTAATTAATTAATTAATTAAT 1620
Db 1561 AATTCAATCATCTGAGCGGAGAAATCGCTCCAAATATTAATTAATTAATTAATTAATTAAT 1620
QY 1621 ACAGACCTTGTCAATTTGTAGCGGATGAGAGCTTGGTGACTTATTAAGGCAAG 1680
Db 1621 ACAGACCTTGTCAATTTGTAGCGGATGAGAGCTTGGTGACTTATTAAGGCAAG 1680
QY 1681 GCATTAGAACCAATATAAAGCTCGAGATGTGCTGGGAAATGACGGTTTCAATTAATTTGGA 1740
Db 1681 GCATTAGAACCAATATAAAGCTCGAGATGTGCTGGGAAATGACGGTTTCAATTAATTTGGA 1740
QY 1741 GTACCTTTGCCAGAGAACCAACAGATGATGATCCCTTCGAAACATTTTGTCTAGATAAT 1800
Db 1741 GTACCTTTGCCAGAGAACCAACAGATGATGATCCCTTCGAAACATTTTGTCTAGATAAT 1800
QY 1801 GTAGCTTCTATCTGCTCANTTACCACGCTGGAAGCTTGTGGGAAAGTCTTGATGACAGT 1860
Db 1801 GTAGCTTCTATCTGCGCATTTACCACGCTGGAAGCTTGTGGGAAAGTCTTGATGACAGT 1860
QY 1861 TTTCCGTGTTATGCGGATCAAGCATTAACGCTTGTGATGCTCCACATTTCCCTTACGAA 1920
Db 1861 TTTCCGTGTTATGCGGATCAAGCATTAACGCTTGTGATGCTCCACATTTCCCTTACGAA 1920
QY 1921 CCAAAACAGCCATCTCAGGCTTCTATCTGATTTAGGAAGTATGATGACACATTTCC 1980
Db 1921 CCAAAACAGCCATCTCAGGCTTCTATCTGATTTAGGAAGTATGATGACACATTTCC 1980
QY 1981 AACCACTAGAGATTTCTCAATATTTTGTGTTGTTCTTAATGAATCTCTGCGCGCATTTGCTC 2040
Db 1981 AACCACTAGAGATTTCTCAATATTTTGTGTTGTTGTTAAATGAATCTCTGCGCGCATTTGCTC 2040
QY 2041 TTTTATTAATTAATTAATTAATTTTGTGTTTGTGTTTGTGCGCAGTATGTCGCTTCC 2100
Db 2041 TTTTATTAATTAATTAATTAATTTTGTGTTTGTGTTTGTGCGCAGTATGTCGCTTCC 2100
QY 2101 AAGAAAGGTCAATCCGGTTGGAGGCTATTCATAATTAATTAATTAATTAATTAATTAATTAAT 2160
Db 2101 AAGAAAGGTCAATCCGGTTGGAGGCTATTCATAATTAATTAATTAATTAATTAATTAATTAAT 2160
QY 2161 CG 2162
Db 2161 CG 2162

RESULT 2
US-10-046-232-21
; Sequence 21, Application US/10046232
; Publication No. US2003011909A1
; GENERAL INFORMATION:
; APPLICANT: Helmut SCHWAB
; APPLICANT: Anton GLIEDER
; APPLICANT: Christoph KRATKY
; APPLICANT: Ingrid DREVENY
; APPLICANT: Peter POCHLAUER
; APPLICANT: Wolfgang SKRANC
; APPLICANT: Herbert MAYRHOFER
; APPLICANT: Irma WIRTH
; APPLICANT: Rudolf NEUHOFFER
; APPLICANT: Rodolfo BONA
; TITLE OF INVENTION: New genes containing a DNA sequence coding for a hydroxynitrile
; TITLE OF INVENTION: recombinant proteins derived therefrom and having hydroxynitrile
; TITLE OF INVENTION: thereof
; FILE REFERENCE: 2001-1882A/LC/01553
; CURRENT APPLICATION NUMBER: US/10/046,232
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: A60/2001
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: A523/2001
; PRIOR FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 1632
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: DNA coding for hybrid pro
; OTHER INFORMATION: PamNLSxGOX
US-10-046-232-21

Query Match 58.8%; Score 1272; DB 15; Length 1632;
Best Local Similarity 88.0%; Pred. No. 0;
Matches 1485; Conservative 0; Mismatches 0; Indels 203; Gaps 1;
QY 281 TACACGCCCTGATACAGCTCGGAGGATCATATGACTACATTGTGTAATCGGTGAGGA 340
DB 94 TACACGCCCTGATACAGCTCGGAGGATCATATGACTACATTGTGTAATCGGTGAGGA 153
QY 341 ACATCAGGCTGCTCATGCGAGCACTTTATCAGAAAAATACAGGCTGCTTCTCTAGAA 400
DB 154 ACATCAGGCTGCTCATGCGAGCACTTTATCAGAAAAATACAGGCTGCTTCTCTAGAA 213
QY 401 AGAGGCACTATTGTACAGAAATACCCGAAACAGCTGTGCTCAGATGGGTTGCAATAAT 460
DB 214 AGAGGCACTATTGTACAGAAATACCCGAAACAGCTGTGCTCAGATGGGTTGCAATAAT 273
QY 461 CTGACGCAACAGATGATGAAAGACGCGAGTTGAAGGTTCTGTCCGAGAGTGCATT 520
DB 274 CTGACGCAACAGATGATGAAAGACGCGAGTTGAAGGTTCTGTCCGAGAGTGCATT 333
QY 521 GATAATGTGCGAGCCAGGCTCTCGGTGGCCAGCAATCAATCAATGAGGCTCTACGCC 580
DB 334 GATAATGTGCGAGCCAGGCTCTCGGTGGCCAGCAATCAATCAATGAGGCTCTACGCC 393
QY 581 AGAGCTAACCTTCAATTCATAGTCAAAAGGAATGAAATGGGACCTGGATTGGTCAAT 640
DB 394 AGAGCTAACCTTCAATTCATAGTCAAAAGGAATGAAATGGGACCTGGATTGGTCAAT 453
QY 641 AAGCATATGATGGGTTGAGAGCCCATTTGTGTGTAAGCCAAATCAATCAATCTTGGCAA 700
DB 454 AAGCATATGATGGGTTGAGAGCCCATTTGTGTGTAAGCCAAATCAATCAATCTTGGCAA 513
QY 701 TCTGTTATAGGAGGATCTTCTGAGCGGGTATCTTCCAGACATGATGATTTAGTTTG 760
DB 514 TCTGTTATAGGAGGATCTTCTGAGCGGGTATCTTCCAGACATGATGATTTAGTTTG 573

QY 761 GATCAGAGCAGGAACTAGACTCACCAGCTCAACTTTTGAACAATATGGAACCGGACAT 820
DB 574 GATCAGAGCAGGAACTAGACTCACCAGCTCAACTTTTGAACAATATGGAACCGGACAT 633
QY 821 GCGGCTGATGAATCGCTTAATAAAGGAGACCTTAATTAATCTTGTAGTGTGAGTTCAGGCC 880
DB 634 GCGGCTGATGAATCGCTTAATAAAGGAGACCTTAATAATCTTGTAGTGTGAGTTCAGGCC 693
QY 881 TCAGTAGAGAAGATCCTCTCTCTTCCAAATACATCAAGTATGTTGCATCAGTGAATTTA 940
DB 694 TCAGTAGAGAAGATCCTCTCTCTTCCAAATACATCAAGTATGTTGCATCAGTGAATTTA 730
QY 941 ATGGTAGCTCCTAGTTTGTCTCATGCTGCACTCGAAATTAATTTATTTATCATTTTAAATA 1000
DB 731 ----- 730
QY 1001 CTACAGATAGTGTGAAGTCTCATATTTCCCTTCCATATTTCCCAAAATTTCCATAAACA 1060
DB 731 ----- 730
QY 1061 AAACCTTCCAAATCTCTCTCGTTTGTAGTTTGAACAATAATATAAGCTATTTCTTAATGAG 1120
DB 731 ----- 730
QY 1121 ATTTGTAGCTATTTGAGTCAATATATACGGATTTCTGATGGAACCTCTCATCAGGCAATTTG 1180
DB 731 ATTTGTAGCTATTTGAGTCAATATATACGGATTTCTGATGGAACCTCTCATCAGGCAATTTG 790
QY 1181 TACGGGTAAACGAGAACTTATTTGTAGTGAAGGACCAATCGGACGCTCTGAGTCTTAC 1240
DB 791 TACGGGTAAACGAGAACTTATTTGTAGTGAAGGACCAATCGGACGCTCTGAGTCTTAC 850
QY 1241 TACTTAGTGGGCTTGGACAGAGTCTTACCTATCTTCTCAACATCAGTGTGTTACG 1300
DB 851 TACTTAGTGGGCTTGGACAGAGTCTTACCTATCTTCTCAACATCAGTGTGTTACG 910
QY 1301 CGAATCTTATGTTGGGCAAGTTGTGATGACAAATCTCTGTAATTTCTTAATATTTTGC 1360
DB 911 CGAATCTTATGTTGGGCAAGTTGTGATGACAAATCTCTGTAATTTCTTAATATTTTGC 970
QY 1361 CCCCAGAAATCCAAATGCAAGCTCTGTTGTAACCTGTTTAGGCAATTAAGAGTGAATTAATC 1420
DB 971 CCCCAGAAATCCAAATGCAAGCTCTGTTGTAACCTGTTTAGGCAATTAAGAGTGAATTAATC 1030
QY 1421 AAGTTTCTCTGTCAAGCTTGGCAATTTCCACTCCACCTTTAGTCTTTTCTTCTCAACAT 1480
DB 1031 AAGTTTCTCTGTCAAGCTTGGCAATTTCCACTCCACCTTTAGTCTTTTCTTCTCAACAT 1090
QY 1481 CTTACCCCTCCCAAAATTCGACTTTTGTCTCATATTTGTAGCCAAAGTTCCAGGACCATTTG 1540
DB 1091 CTTACCCCTCCCAAAATTCGACTTTTGTCTCATATTTGTAGCCAAAGTTCCAGGACCATTTG 1150
QY 1541 CTCATGTTCTGTCAAGCTTAAATTCATCATCTGAGTGAAGTCCCTCCAAATTAAT 1600
DB 1151 CTCATGTTCTGTCAAGCTTAAATTCATCATCTGAGTGAAGTCCCTCCAAATTAAT 1210
QY 1601 TCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1660
DB 1211 TCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1270
QY 1661 GTGACTTATTAAGGCAAAAGGCAATTAAGCAATATATAAGCTCGAGATGTGCTGGGAATTTG 1720
DB 1271 GTGACTTATTAAGGCAAAAGGCAATTAAGCAATATATAAGCTCGAGATGTGCTGGGAATTTG 1330
QY 1721 AGGTTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1780
DB 1331 AGGTTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1390
QY 1781 AAACATTTTGTCTAGATAATGTAGCTTCTCATCTGCGATTACCCAGGTCGAGGCTTTGTTG 1840
DB 1391 AAACATTTTGTCTAGATAATGTAGCTTCTCATCTGCGATTACCCAGGTCGAGGCTTTGTTG 1450


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; PRIOR APPLICATION NUMBER: A60/2001
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: A523/2001
; PRIOR FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 68
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: Synthetic oligonucleotide
US-10-046-232-4

Query Match      3.1%; Score 68; DB 15; Length 68;
Best Local Similarity 100.0%; Pred. No. 8.4e-08;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 CTATTGTTGTCATCTTCTTCTTCATCTTCAGTATTCAGAGTTCAGTTCGCC 99
Db 1 CTATTGTTGTCATCTTCTTCTTCATCTTCAGTATTCAGAGTTCAGTTCGCC 60

QY 100 AATCTTC 107
Db 61 AATCTTC 68

RESULT 6
US-09-770-961-453
; Sequence 453, Application US/09770961
; Publication No. US20030115639A1
; GENERAL INFORMATION:
; APPLICANT: Goriach, Jörn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kriker, Ted
; APPLICANT: Slader, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2026 (PARA-015PRV)
; CURRENT APPLICATION NUMBER: US/09/770,961
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,466
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 453
; LENGTH: 499
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-961-453

Query Match      3.1%; Score 66.6; DB 11; Length 499;
Best Local Similarity 55.4%; Pred. No. 6.5e-07;
Matches 129; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 1180 GTACGGCGTACCGGAGAGTATTGTTAGTGCAGGCAATCGGAGCGCTCAGCTTCTA 1239
Db 137 GAAGGCGCTTGATGATGATCATCTTCATCGGCCGGAACCCCTAGGAGCCCAACTTCTT 196
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QY 1240 CTACTTAGTGGCGTTGGACACAGAGTCTTACCTATCTTCTCAACATCACAGTGTTCAG 1299
Db 197 ATGCTAAGTGGTGTGGCCCATCGCTCAATTCAGGCCCAACAATCACAGTGTGTGATG 256
QY 1300 CCGAATCCTTATGTTGGGCGAGTGTGTGATGACAAATCTCTGTAATTTCAATTAATTTG 1359
Db 257 GACCAGCCTCATGTGGTCAAGGCGATGTATGACAAACCCCTATGAATGCCGTGTCTCTCT 316
QY 1360 CCCCCAAATCCAATTAAGAGCTCTGTTGTAAGTCTTTTAGGCATTAAGAGTGA 1412
Db 317 TCTCCAGTCCCGGTGGAGGCTCTACTCAATGAGGTGTGTGGATTACCGGGGA 369

RESULT 7
US-10-046-232-9/c
; Sequence 9, Application US/10046232
; Publication No. US20030119099A1
; GENERAL INFORMATION:
; APPLICANT: Helmut SCHWAB
; APPLICANT: Anton GLIEDER
; APPLICANT: Christoph KRATKY
; APPLICANT: Ingrid DREVENY
; APPLICANT: Peter FOCHLAUER
; APPLICANT: Wolfgang SKRANC
; APPLICANT: Herbert MAYRHOFER
; APPLICANT: Irma WIRTH
; APPLICANT: Rudolf NEUHOFFER
; APPLICANT: Rodolfo BONA
; TITLE OF INVENTION: New genes containing a DNA sequence coding for a hydroxynitrile
; TITLE OF INVENTION: recombinant proteins derived therefrom and having hydroxynitril
; FILE REFERENCE: 2001-1882A/LC/01553
; CURRENT APPLICATION NUMBER: US/10/046,232
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: A60/2001
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: A523/2001
; PRIOR FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 73
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: Synthetic oligonucleotide
US-10-046-232-9

Query Match      3.0%; Score 65; DB 15; Length 73;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2097 CTGCAAGAAAGCTCAATCGGTTGGAGGCTTATTCATATATTCAGAGTCCATCTGAAGA 2156
Db 73 CTGCAAGAAAGCTCAATCGGTTGGAGGCTTATTCATATATTCAGAGTCCATCTGAAGA 14
QY 2157 ATTCC 2161
Db 13 ATTCC 9

RESULT 8
US-09-770-445-404/c
; Sequence 404, Application US/09770445
; Patent No. US2002023281A1
; GENERAL INFORMATION:
; APPLICANT: Goriach, Jörn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
```

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; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Bedford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurlban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; TITLE OF INVENTION: thaliana
; FILE REFERENCE: 2023US (PARA-012PRV)
; CURRENT APPLICATION NUMBER: US/09/770,445
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/178,472
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 404
; LENGTH: 925
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-445-404

Query Match      2.8%; Score 60.6; DB 9; Length 925;
Best Local Similarity 53.6%; Pred. No. 3.6e-05;
Matches 126; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

QY 1749 GCCAGAGAACCAACAGATGATGCTTCGAAACATTTTGTCTAGATATAGTCTTC 1808
Db 571 GCCAAGCACTGAAGCATACCAATCAATGGCTCAGTCTCGCAAGACACTGTGTGTCAC 512
QY 1809 ATACTGTCATTACCACGGTGAAGCTTTGTGGAAAGTCTTCATGACAGTTCGGTGT 1868
Db 511 AATCTGGCACTACCATGGTGGATGCTCTGTGGGTAAGTGTGAGCCCTAACCGCAAGT 452
QY 1869 TATGGGATCAAGCATTAACGGTGTGTGATGCTCCCTCCACTTCCTTACGAACCAACAG 1928
Db 451 TCTTGGTGTGACAGCGTCAAGTATTAATGTTTCAACGTTTGACGAGTCTCCAGAAC 392
QY 1929 CCATCTCTCAGGCTTCTATCTGATGTTAGGAAGTATGTGATGACACTTCCAAAC 1983
Db 391 CAACCCGCAAGCTACTATGATGATGATGGGAAGTAAATCAAAATCATTACCAAC 337

RESULT 9
US-09-294-093B-3196
; Sequence 3196, Application US/09294093B
; Patent No. US20010051335A1
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath, V.
; APPLICANT: Ito, Laura, Y.
; APPLICANT: Sherman, Bradley, K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
; FILE REFERENCE: PL-0009 US
; CURRENT APPLICATION NUMBER: US/09/294,093B
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/082,567
; PRIOR FILING DATE: April 21, 1998
; NUMBER OF SEQ ID NOS: 6207
; SOFTWARE: PERL Program
; SEQ ID NO 3196
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20010051335A1 700347360H1
US-09-294-093B-3196
; Location: 108
; OTHER INFORMATION: a, t, c, g, or other
US-09-294-093B-3196

Query Match      2.7%; Score 59.4; DB 9; Length 300;
Best Local Similarity 61.1%; Pred. No. 3.7e-05;
Matches 96; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 1812 CTGGCATTACCAACGGTGGAGCCTTGTGGAAAGTCTTCGATGACAGATTTCCGTCTTAT 1871
Db 119 CTGGCATTATCAAGTGGTGGTGCATGATGAGGAGGTGGTTCACCACTTACCGGTGCT 178
QY 1872 GGGGATCAAGCAATACCGGTGTGTGATGCCCTCCACTTTCCTTACGAACCAACAGCCA 1931
Db 179 TGGAGTTTCAGGTCCTCCGGTGGTTCAGCGCTCAATATTTCTAAATGCCAGGGACCA 238
QY 1932 TCTCAGGGCTTCTATCTATCTGATGTTAGGAAGGTATGTG 1968
Db 239 CCCTCAAGCTACAGTTATGATGATGGCAGATATATG 275

RESULT 10
US-09-294-093B-1444
; Sequence 1444, Application US/09294093B
; Patent No. US20010051335A1
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath, V.
; APPLICANT: Ito, Laura, Y.
; APPLICANT: Sherman, Bradley, K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
; FILE REFERENCE: PL-0009 US
; CURRENT APPLICATION NUMBER: US/09/294,093B
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/082,567
; PRIOR FILING DATE: April 21, 1998
; NUMBER OF SEQ ID NOS: 6207
; SOFTWARE: PERL Program
; SEQ ID NO 1444
; LENGTH: 276
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20010051335A1 700344337H1
US-09-294-093B-1444

Query Match      2.7%; Score 58.6; DB 9; Length 276;
Best Local Similarity 57.0%; Pred. No. 5.8e-05;
Matches 126; Conservative 0; Mismatches 94; Indels 1; Gaps 1;

QY 1748 TGCCAGAGAACCAACAGATGATGATGCTTCGAAACATTTTGTCTAGATATAGTCTT 1807
Db 53 TACCGAGCATACAAATGACAGATTCCTGGAGCAGTTTTCGAGACACTGTGATCA 112
QY 1808 CATATCGCATTAACCAACGGTGAAGCCTTGTGGAAAGTCTTCGATGACAGTTCGGTG 1867
Db 113 CCATCTGGCATTAATCATGCTGGTGCATGATGAGGAGGTGGTTCACCACTTACCGGG 172
QY 1868 TTATGGGATCAAGCATTAACGGTGTGTGATGCTCCACTTCCTTACGAACCAACACA 1927
Db 173 TGTCTGGAGTTTCAGGTCCTCCGGTGGTTCAGCGCTCAATATTTCTAAATCGCC-AGGA 231
QY 1928 GCCATCTCTCAGGGCTTCTATCTGATGTTAGGAAGGTATGTG 1968
Db 232 CCACCTCAAGCTACAGTTATGATGATGGCAGATATATG 272

RESULT 11
US-09-770-444-909/c
; Sequence 909, Application US/09770444
; Patent No. US2002023280A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jorn

```

```
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; TITLE OF INVENTION: thaliana
; FILE REFERENCES: 2027 (PARA-016PRV)
; CURRENT APPLICATION NUMBER: US/09/770,444
; PRIOR FILING DATE: 2001-01-26
; PRIOR FILING DATE: 60/178,502
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 909
; LENGTH: 441
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-444-909

Query Match          2.5%; Score 54.6; DB 9; Length 441;
Best Local Similarity 56.4%; Pred. No. 0.00086;
Matches 102; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 1795 GATATGTAGCTCATCTGCGGATCAAGCATTACGGTTGTTGATCCCTCCACTTCCCT 1854
    |||||
Db 441 GATACCGTGATGACTATTATCATCTACCATGAGGTGTCAAGTTGGAAAAGTGGTCGAC 382

QY 1855 GACAGTTTCGTTGTTGGGATCAAGCATTACGGTTGTTGATCCCTCCACTTCCCT 1914
    |||||
Db 381 AACATTTACAAATATAGGGTGTGATCTTTGAGATCATCATGATCCAGTTTC 322

QY 1915 TAGCAACCAAGCCATCTCAGGGCTTCTATCTGATGTAGGAAGGTATGTATGTCAC 1974
    |||||
Db 321 AAGTCTCGGGGACTAATCCACAGCCACAAATCATCATGCTCGGAGATATATGGGGCAG 262

QY 1975 A 1975
Db 261 A 261

RESULT 12
US-09-878-574-207
; Sequence 207, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCES: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; PRIOR FILING DATE: 2001-12-21
; PRIOR FILING DATE: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 207
; LENGTH: 267
; TYPE: DNA
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; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-053-Q1-B1-G4
US-09-878-574-207

Query Match          2.4%; Score 51.2; DB 10; Length 267;
Best Local Similarity 59.7%; Pred. No. 0.005;
Matches 86; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 1825 GGTGAAGCCTTGTGGGAAAGTCTTGATCAGAGTTTCCTGTTATGGGATCAAGCA 1884
    |||||
Db 1 GGAGGGTGCCCAATCTGGTAAAGTTGTCATCATATATATAGGTTATGGTTGAGCT 60

QY 1885 TTACGCGTTGTGATGCTCCACTTCCCTTACGAACCAACAGCCATCTTCAGGGCTTC 1944
    |||||
Db 61 TTGAGGGTAATTGATGGATCCACTTTTCATGGCTCACCGGGTACAAATCCTCAAGCTACT 120

QY 1945 TATCTGATGTTAGGAGGTATGTG 1968
    |||||
Db 121 GTAATGATGCTTGGGAAGGTATATG 144

RESULT 13
US-10-046-232-3
; Sequence 3, Application US/10046232
; Publication No. US20030119099A1
; GENERAL INFORMATION:
; APPLICANT: Helmut SCHWAB
; APPLICANT: Anton GLIEDER
; APPLICANT: Christoph KRATKY
; APPLICANT: Ingrid DREVENTY
; APPLICANT: Peter POCHLAUER
; APPLICANT: Wolfgang SKRANC
; APPLICANT: Herbert MAYRHOFER
; APPLICANT: Irma WIRTH
; APPLICANT: Rudolf NEUHOEFER
; APPLICANT: Rodolfo BONA
; TITLE OF INVENTION: New genes containing a DNA sequence coding for a hydroxynitrile
; TITLE OF INVENTION: recombinant proteins derived therefrom and having hydroxynitril
; FILE REFERENCES: 2001-1882A/LC/01553
; CURRENT APPLICATION NUMBER: US/10/046,232
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: A60/2001
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: A523/2001
; PRIOR FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 64
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: Synthetic oligonucleotide
US-10-046-232-3

Query Match          2.3%; Score 49; DB 15; Length 64;
Best Local Similarity 100.0%; Pred. No. 0.008;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 ATGAGAAATCAACAATGTCAGTTATATATATCTATTTGTGTGATCTCTCTTG 61
    |||||
Db 16 ATGAGAAATCAACAATGTCAGTTATATATATCTATTTGTGTGATCTCTCTTG 64

RESULT 14
US-10-046-232-8/c
; Sequence 8, Application US/10046232
; Publication No. US20030119099A1
; GENERAL INFORMATION:
; APPLICANT: Helmut SCHWAB
; APPLICANT: Anton GLIEDER
; APPLICANT: Christoph KRATKY
```


GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2003, 15:05:47 ; Search time 130 Seconds
(without alignments)
7340.541 Million cell updates/sec

Title: US-10-046-232-19
Perfect score: 2162
Sequence: 1 ggaattcacaataggagaa.....agtcctatggaagaattccg 2162

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgm2_6/ptodata/2/ina/5A COMB.seq.*
2: /cgm2_6/ptodata/2/ina/5B COMB.seq.*
3: /cgm2_6/ptodata/2/ina/6A COMB.seq.*
4: /cgm2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgm2_6/ptodata/2/ina/6CTUS COMB.seq.*
6: /cgm2_6/ptodata/2/ina/backfilea.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58.8	2.7	7218	1	US-08-232-463-14
2	45	2.1	1863	3	US-09-199-229-1
3	45	2.1	1863	3	US-09-443-087-1
4	45	2.1	1863	4	US-09-687-298-1
5	41.2	1.9	1497	4	US-09-220-132-94
6	40.8	1.9	7218	1	US-08-232-463-14
7	40	1.9	6527	4	US-09-492-308A-3
8	39.8	1.8	1737	4	US-09-328-352-1553
9	38.4	1.8	3431	4	US-09-155-078-1
10	38	1.8	2351	4	US-09-620-312D-848
11	36.8	1.7	1830121	4	US-09-557-884-1
12	36.8	1.7	1830121	4	US-09-643-990A-1
13	36.2	1.7	168575	4	US-09-426-290-1
14	36	1.7	1194	4	US-09-601-198-77
15	36	1.7	3600	3	US-08-894-731-1
16	35.8	1.7	10569	4	US-08-961-527-57
17	35.8	1.7	1664976	4	US-08-916-421B-1
18	35.6	1.6	2277	1	US-08-676-967-2
19	35.6	1.6	2277	1	US-08-676-974-2
20	35.6	1.6	2277	2	US-09-098-487-2
21	35.4	1.6	795	4	US-09-134-001C-943
22	35.4	1.6	19718	4	US-08-961-527-99
23	35.2	1.6	1292	4	US-09-843-164A-3
24	35.2	1.6	3216	2	US-08-828-007-1
25	35.2	1.6	3231	3	US-08-632-806A-7
26	35.2	1.6	1830121	4	US-09-557-884-1
27	35.2	1.6	1830121	4	US-09-643-990A-1

28	35	1.6	294	4	US-09-134-001C-2110	Sequence 2110, Ap
29	34.8	1.6	2058	2	US-08-749-391-1	Sequence 1, Appli
30	34.8	1.6	2058	3	US-09-390-200-1	Sequence 1, Appli
31	34.6	1.6	854	3	US-08-998-416-534	Sequence 534, App
32	34.6	1.6	2781	3	US-08-749-522-4	Sequence 4, Appli
33	34.6	1.6	4854	4	US-08-961-527-178	Sequence 178, App
34	34.4	1.6	3509	4	US-09-255-829-19	Sequence 19, Appli
35	34.2	1.6	2037	1	US-08-844-085-1	Sequence 1, Appli
36	34.2	1.6	4259	2	US-08-816-155B-2	Sequence 2, Appli
37	34.2	1.6	4259	3	US-09-079-587-2	Sequence 2, Appli
38	34.2	1.6	4344	4	US-09-601-198-165	Sequence 165, App
39	34	1.6	1664976	4	US-08-916-421B-1	Sequence 1, Appli
40	33.8	1.6	390	1	US-08-844-085-3	Sequence 3, Appli
41	33.8	1.6	747	3	US-08-591-468-1	Sequence 1, Appli
42	33.8	1.6	747	5	PCT-US94-06430-1	Sequence 1, Appli
43	33.8	1.6	829	3	US-08-591-468-5	Sequence 5, Appli
44	33.8	1.6	829	5	PCT-US94-06430-5	Sequence 5, Appli
45	33.8	1.6	1277	3	US-09-347-803-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHREIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 INMGU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
; US-08-232-463-14

Query Match 2.7%; Score 58.8; DB 1; Length 7218;

Db 940 GGGGAAACCTTGTGATCACCAGACCATCATCA 976

RESULT 5

US-09-220-132-94/c

; Sequence 94, Application US/09220132

; Patent No. 6506607

; GENERAL INFORMATION:

; APPLICANT: Shyjan, Andrew W.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT

; TITLE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 07334-074001

; CURRENT APPLICATION NUMBER: US/09/220.132

; CURRENT FILING DATE: 1998-12-23

; PRIOR APPLICATION NUMBER: US 60/079,303

; PRIOR FILING DATE: 1998-03-25

; PRIOR APPLICATION NUMBER: US 60/068,821

; PRIOR FILING DATE: 1997-12-24

; NUMBER OF SEQ ID NOS: 191

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 94

; LENGTH: 1497

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc.feature

; LOCATION: (1)..(1497)

; OTHER INFORMATION: n = A,T,C or G

US-09-220-132-94

Query Match

Best Local Similarity 27.68; Score 41.2; DB 4; Length 1497;

Matches 64; Conservative 65; Mismatches 103; Indels 0; Gaps 0;

QY 130 TCAGTATCTTTAAACGACAAATGTGTAGATTATTAATAAGAAACTGACACAGTAG 189

Db 589 TAAATATATCATTTAAAAAATATTTCTAGGGGATCATGAAGTARTGAGGTATTAC 530

QY 190 TGCAGAAACAGCTAATTAGATGCTATGTTGAAATAATCTTTTCTCTTACATATA 249

Db 529 ATCTMRRRAARRWTGGKAWTAAATKRAACMAAARKMCMAMYYTTCMVCARR 470

QY 250 TTTTGCAGATTAGCTACTTGAAGTTGTGTACACGCCACATGATACAGCTCGGAAG 309

Db 469 WTKCCMATTWMSKAWCYTKSYTWRRAWKSCCCMRGSCYKTKMARSCYKGRMY 410

QY 310 ATCATATGACTACATTTGTAATCGGTGGAGAACATCAGGGTGTCCATTGGCA 361

Db 409 TGRAAAWTAAWTKKKTTMWARWKKKSYGGRWKKSCYVTTTCMRKTYCM 358

RESULT 6

US-08-232-463-14/c

; Sequence 14, Application US/08232463

; Patent No. 5670367

; GENERAL INFORMATION:

; APPLICANT: DORNER, F.

; APPLICANT: SCHEIFLINGER, F.

; APPLICANT: FALKNER, F. G.

; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS

; NUMBER OF SEQUENCES: 52

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 1800 Diagonal Road, Suite 500

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22313-0299

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/232,463

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/935,313

; FILING DATE:

; APPLICATION NUMBER: EP 91 114 300.6

; FILING DATE: 26-AUG-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: BENT, Stephen A.

; REGISTRATION NUMBER: 29,768

; REFERENCE/DOCKET NUMBER: 30472/114 IMMU

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703)836-9300

; TELEFAX: (703)683-4109

; TELEX: 899149

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7218 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; CLONE: pTZ9pt-Fls

; US-08-232-463-14

Query Match 1.9%; Score 40.8; DB 1; Length 7218;

Best Local Similarity 11.4%; Pred. No. 0.18; Mismatches 234; Indels 0; Gaps 0;

Matches 57; Conservative 207;

QY 134 TATTCATTAAACAGCAAAATGTGTAGATTATAATTAAGAAACTGACACAGTAGTGCA 193

Db 1470 TATCAAGTAGTAAAGAGATAGAAGATTTGGTACRRRRRRRRRRRRRRRRRRRR 1411

QY 194 AGAAACAAGCTAATTTAGATGATGCTTGAATAAATCTTTTCATCTCTTCACATATATTT 253

Db 1410 RRR 1351

QY 254 GCAGATTATTAGTACTTGAAGTTTGTGTACAGCCACTGATACAGCTCGGAAGATCA 313

Db 1350 RRR 1291

QY 314 TAAGACTACATGTAATCGGTGGAGAACATCAGGGTGTCCATTGGCAGCAACTTATCA 373

Db 1290 RRR 1231

QY 374 GAAAAATACAGGTGCTTCTTCTAGAAAGAGGACTATTGTACGAATACCCGAACAG 433

Db 1230 RRR 1171

QY 434 TTGACTGCAGATGGGTTTGCATATAATCTGCAGCAACAAGATGATGGAAGACGCCAGTT 493

Db 1170 RRR 1111

QY 494 GAAAGTTGCTGTCGGAAGATGGCATTGATATGTGAGCAGCATCTCGGTGGCAGC 553

Db 1110 RRR 1051

QY 554 ACCATAATCAATGAGGGCTCTAGCCAGACTAACATTTCATTCTATAGTCAACAGGA 613

Db 1050 ACTGACGCCAAGCTCGGAATTAATCTGTGAGGTATGGAACGAAGAAAAATAGTT 991

QY 614 ATTGAATGGGACCTGGAT 631

Db 990 ATAGTAGCCGACTCGAT 973

RESULT 7

US-09-492-308A-3/c

; Sequence 3, Application US/09492308A

; Patent No. 6573430

GENERAL INFORMATION:
 APPLICANT: Bradley, DJ
 Carpenter, R
 Coen, ES
 TITLE OF INVENTION: Flowering genes
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Nixon & Vanderhye PC
 STREET: 8th Floor, 1100 No. 6573430th Glebe Road
 CITY: Arlington
 STATE: Virginia
 COUNTRY: United States of America
 ZIP: 22201-4714
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/492,308A
 FILING DATE: 27-Jan-2000
 CLASSIFICATION: 435 (Preliminary)
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/043,029
 FILING DATE: 13-MAR-1998
 APPLICATION NUMBER: PCT/GB96/02276
 FILING DATE: 13-SEP-1996
 APPLICATION NUMBER: GB 9518731.6
 FILING DATE: 13-SEP-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Mary J. Wilson
 REGISTRATION NUMBER: 32,955
 REFERENCE/DOCKET NUMBER: 620-93
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4000
 TELEFAX: (703) 816-4100
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6527 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYDROTHERMAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Antirrhinum majus
 IMMEDIATE SOURCE:
 CLONE: CEN GENOMIC
 POSITION IN GENOME:
 UNITS: bp
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Query Match 1.9%; Score 40; DB 4; Length 6527;
 Best Local Similarity 49.5%; Pred. No. 0.29;
 Matches 103; Conservative 0; Mismatches 105; Indels 0; Gaps 0;
 QY 77 ATTGAGGTTCACTCGGTCGCAATCTTCTGCTGTAATTTCCATCTTCAGTAT 136
 DB 1782 ATGCTTATCTTCCCTATTAATTAAGTTTATACCTGGCGGTACATATATCTTTGCCAATAT 1723
 QY 137 TCATTTAAGCAGCAAAATGTAGATTTTATTAATTAAGAACTGACACAAGTAGTGAAGA 196
 DB 1722 TCAGTTTACATACATCAATTTAGATATATTAATTAATTAAGTGTGACCATATATTTGTGA 1663
 QY 197 AACAGCTAATTTAGATCATCTTTGAAATAAATCTTTCATCTTTCACATATATTTGCA 256
 DB 1662 AAAAGTATGAGATACCAATCATCTGTTCAAGAAATTTACACCAACATATTTTTCATTA 1603
 QY 257 GATTTTACCTCTCAAGTTTGTGTACA 284
 DB 1602 GATATTTTCAATTTGAACACTCCTTTATA 1575

RESULT 8
 US-09-328-352-1553
 Sequence 1553, Application US/09328352
 Patent No. 6562958
 GENERAL INFORMATION:
 APPLICANT: Gary L. Breton et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: GTC99-03PA
 CURRENT APPLICATION NUMBER: US/09/328,352
 CURRENT FILING DATE: 1999-06-04
 NUMBER OF SEQ ID NOS: 8252
 SEQ ID NO 1553
 LENGTH: 1737
 TYPE: DNA
 ORGANISM: Acinetobacter baumannii
 US-09-328-352-1553

Query Match 1.8%; Score 39.8; DB 4; Length 1737;
 Best Local Similarity 52.0%; Pred. No. 0.17;
 Matches 89; Conservative 0; Mismatches 82; Indels 0; Gaps 0;
 QY 1128 AGCTATTGGAGTCATATATACGGAATTCCTGATGGAACCTCTCATCAGGCAATTTGTACGGG 1187
 DB 780 AGCAATTTGGTGTGAATATACATTTATTTGGTGTGATCAAAACAACTTGCAACGTGCTTAGT 839
 QY 1188 TAACGGAGAAATTTATTTAGTCAGGCAACAACTCGAAGCCTCAGCTTCTACTACTTAG 1247
 DB 840 TAACGGCAAGTATTTACTTTGTGCGGCGCAATTTGGTTCACGCCAAATTTACAGGTTTC 899
 QY 1248 TGGGTTGGACCAAGAGTCTTACCTATCTTCTCAACATCAGTGTGTTCA 1298
 DB 900 AGGTGTAGTCAAAGCACCTTCTTAAATCAATGACATTTGTTGTTCA 950

RESULT 9
 US-09-155-078-1
 Sequence 1, Application US/09155078
 Patent No. 6312688
 GENERAL INFORMATION:
 APPLICANT: POUSTKA, Annemarie
 APPLICANT: KIOSCHIS, Petra
 APPLICANT: LAPORTE, Jocelyn
 APPLICANT: HU, Ling Jia
 APPLICANT: MANDEL, Jean Louis
 APPLICANT: DAHL, Niklas
 TITLE OF INVENTION: TYROSINE-PHOSPHATASE-RELATED PROTEIN
 FILE REFERENCE: 012627-010
 CURRENT APPLICATION NUMBER: US/09/155,078
 CURRENT FILING DATE: 1999-03-02
 EARLIER APPLICATION NUMBER: PCT/DE97/00592
 EARLIER FILING DATE: 1997-03-21
 EARLIER APPLICATION NUMBER: DE 196 11 234.6
 EARLIER FILING DATE: 1996-03-21
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 1
 LENGTH: 3431
 TYPE: DNA
 ORGANISM: German-type microorganism & cell cul.
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1) .. (1863)
 US-09-155-078-1

Query Match 1.8%; Score 38.4; DB 4; Length 3431;
 Best Local Similarity 55.1%; Pred. No. 0.6;
 Matches 75; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
 QY 933 GATATTTAATGCTAGCTCCTAGTTTGTGATGCTGCACTCGAAATATTTATTTATCATT 992
 DB 2444 GAAATTTAGGGGAGAAATGTTTTCCTTAATTTCCAGAGGACCTATTTTATTTT 2503

the Haemophilus influenzae Rd Genome, Fragments
thereof, and Uses Thereof

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS: 1

ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville,
STATE: MD
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/643,990A
FILING DATE: 23-Aug-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,429

FILING DATE: 1995-06-07

APPLICATION NUMBER: 08/426,787

FILING DATE: 1995-04-21

ATTORNEY/AGENT INFORMATION:

NAME: Kenley K. Hoover

REGISTRATION NUMBER: 40,302

REFERENCE/DOCKET NUMBER: PB186P1C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 301-610-5790

TELEFAX: 310-309-8439

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1830121 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-643-990A-1

Query Match 1.7%; Score 36.8; DB 4; Length 1830121;
Best Local Similarity 51.9%; Pred. No. 37;
Matches 83; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 1240 CTACTTGTGGTGGACCGAGCTTACTATCTCTCCACATCAGTGTGTCAG 1299
DB 521756 CCACCTTCTGTGTGGAGCTGGCTGCTCAATCGCTAAGAAATGGTGCAAGGTGTG 521815

QY 1300 CGAATCCTTATGTTGGGAGCTTGTGTATGACAACTCCTGTAATTTTCATTAATTTTG 1359
DB 521816 CTAAATCTGCTCCAGCGCAGATTTTATCGAAGATTTATGAGTTGATTTATTT 521875

QY 1360 CCCCACATCCAAATGAAGCTCTGTGTACTGTTTAG 1399
DB 521876 ACACCAATGAACATGAAGCTGAATCTGACTGGGTAG 521915

RESULT 13

US-09-426-290-1

Sequence 1, Application US/09426290

Patent No. 6410712

GENERAL INFORMATION:

APPLICANT: Berglind Ran Olafsdottir

APPLICANT: Jeffrey Gulcher

FILE OF INVENTION: HUMAN NARCOLEPSY GENE

FILE REFERENCE: 2345 2001-000

CURRENT APPLICATION NUMBER: US/09/426,290

NUMBER OF SEQ ID NOS: 24

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 168575

TYPE: DNA

Query Match 1.7%; Score 36; DB 4; Length 1194;

Best Local Similarity 51.2%; Pred. No. 1.8;

Matches 84; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

ORGANISM: Homo Sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (21181)...(21403)

NAME/KEY: CDS

LOCATION: (95252)...(95430)

NAME/KEY: CDS

LOCATION: (101753)...(101996)

NAME/KEY: CDS

LOCATION: (110324)...(110439)

NAME/KEY: CDS

LOCATION: (124058)...(124278)

NAME/KEY: CDS

LOCATION: (127009)...(127130)

NAME/KEY: CDS

LOCATION: (128910)...(129139)

US-09-426-290-1

Query Match 1.7%; Score 36.2; DB 4; Length 168575;

Best Local Similarity 49.4%; Pred. No. 18;

Matches 132; Conservative 0; Mismatches 138; Indels 3; Gaps 1;

QY 909 ATACATCAAGTATGTTGCATCAGTGATATTAAATGAGTACTCTCTAGTTTGTCTCATCTCA 968

DB 109008 ATAAATATATATGATTTATGTTATATATATATATATATATATATATATATATATA 109067

QY 969 CTCGAAATATTTATTTATCAATTTTAAATACTAACAGAAATAGTGTGAAGTCTCATAT- 1027

DB 109068 TATTATTTATATATATCTAAATATATATATATATATATATATATATATATATA 109127

QY 1028 --TTCCCTCCATATTTCCCAATTTCCATAACAAAGCTCCCAATTCCTCTCGTTTA 1085

DB 109128 ACTTA 109187

QY 1086 GTTGCACATAATATAAGCTATTCTCTAATGCAGATTTGTGAGTATTTGGAGTCAATA 1145

DB 109188 TATATATATATATATGCTACTATATATATATATATATATATATATATATATA 109247

QY 1146 TACGATTCCTGATGGAACTCTCATCAGGCATT 1178

DB 109248 TATAAATTTATAATATATATATATATATATATATATATATATATATATAT 109280

RESULT 14

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Sequence 77, Application US/09601198

Patent No. 6531583

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